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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 16, 2004, 01:12:56 ; Search time 1977 Seconds
        (without alignments)
        5696.773 Million cell updates/sec

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Scoring table: BLOSUM62
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              Fgapop 6.0 , Fgapext 7.0
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Searched:      2890132 seqs, 2237290429 residues

Total number of hits satisfying chosen parameters:      5780264

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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                  Listing first 100 summaries

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Database :	Published Applications NA:**	Result No.	Score	Query Match	Length	DB ID	Description
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	13215	100.0	7554	15	US-10-414-692-14	Sequence 14, Appl
2	13215	100.0	8561	15	US-10-174-014-11	Sequence 11, Appl
3	13145	98.5	7627	12	US-10-087-192-653	Sequence 653, App
4	12978	98.2	7521	10	US-09-819-104A-3	Sequence 3, Appl
5	12978	98.2	8686	10	US-09-819-104A-1	Sequence 4, Appl
6	12978	98.2	8686	15	US-10-174-014-4	Sequence 4, Appl
7	10832.5	82.0	7386	10	US-09-819-104A-6	Sequence 6, Appl
8	10832.5	82.0	8544	10	US-09-819-104A-4	Sequence 4, Appl
9	9691.5	73.3	7534	12	US-10-087-192-650	Sequence 650, App
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c 78 562 4.3 24081 14 US-10-132-134-13 Sequence 13, Appli
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c 100 534 4.0 18876 14 US-10-329-079-42 Sequence 42, Appli
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ALIGNMENTS

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RESULT 1
US-10-414-692-14
; Sequence 14, Application US/10414692
; Publication No. US20030228607A1
; GENERAL INFORMATION:
; APPLICANT: X-Ceptor Therapeutics, Inc.
; TITLE OF INVENTION: Screening method and modulators having an improved therapeutic
; FILE OF INVENTION: profile
; FILE REFERENCE: 8012-002-US
; CURRENT APPLICATION NUMBER: US/10/414,692
; PRIOR FILING DATE: 2003-04-14
; PRIOR FILING DATE: 2003-04-14
; PRIOR FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 7554
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-692-14

Alignment Scores:
Pred. No.: 0 Length: 7554
Score: 13215.00 Matches: 2517
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-522-753-5 (1-2517) x US-10-414-692-14 (1-7554)

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Db 3661 AGGCCATCATACCGGCTCCATCCACGGCAGCCAGCTGACGTCCTGTACAAAG 3720
QY 1241 GlyThrIleThrArgIleIleGlyGluAspSerProSerArgLeuAspArgGlyArgGlu 1260
Db 3721 GGCACCATCACAGGATCATCGGCGAGACAGCCGAGTGCCTTGACCCGGCGGAG 3780
QY 1261 AspSerLeuProLysGlyHisValIleTyArgGlyLysGlyHisValLeuSerTyLys 1280
Db 3781 GACAGCTTGCCTCAAGGGCCAGCTCATCTACGAAGGCAGAGGCCACCGTCTTGCTCAT 3840
QY 1281 GluGlyGlyMetSerValThrGlnCysSerLysGluAspGlyArgSerSerGlyPro 1300
Db 3841 GAGGTGGCATGTCTGTGACCATCGAGTGTCCAAAGGAGCAGCGCAGAGCAGCTCAGGACCC 3900
QY 1301 ProHisGluThrAlaAlaProLysArgThrTyAspMetMetGluGlyArgValGlyArg 1320
Db 3901 CCCATGAGAGCGGCGCCCAAGCGCATCTGACATGATGAGGGCCCGCTGGGCGAG 3960
QY 1321 AlaIleSerSerAlaSerIleGluGlyLeuMetGlyArgAlaIleProProGluArgHis 1340
Db 3961 GCATCTCTCAGCAGCATCGAAGTCTCATGGCGCTGTCATCCCGCGGAGCGACAC 4020
QY 1341 SerProHisHisLeuLysGluGlnHisIleArgGlySerIleThrGlnGlyIlePro 1360
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QY 1361 ArgSerTyValGluAlaGlnGluAspTyLeuArgArgGluAlaLysLeuLeuLysArg 1380
Db 4081 CGGTCTCAGTGAGGCGCAGAGGACTTACTGCTCGGAGGCCAAGCTCTTAAAGCGG 4140
QY 1381 GluGlyThrProProProProSerArgAspLeuThrGluAlaTyLysThrGln 1400
Db 4141 GAGGCGACGCTCCGCCCCACCGGCTCAGCGGACCTCAGCGAGGCTACAGACGCGAG 4200
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QY 1421 AlaGlyArgSerIleHisGluIleProArgGluLeuArgHisThrProGluLeuPro 1440
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QY 1441 LeuAlaProArgProLeuLysGluGlySerIleThrGlnGlyThrProLeuLysTyAsp 1460
Db 4321 CTGGCGCGCGCTCAAGGAGGCTCCATCAGCAGGGGACCCCGCTCAAGTACGAC 4380
QY 1461 ThrGlyAlaSerThrThrGlySerLysLysHisAspValArgSerLeuIleGlySerPro 1480
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QY 1521 SerIleAlaArgGlyAlaProValIleValProGluLeuGlyLysProArgGlnSerPro 1540
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QY 1561 ThrMetArgGluProThrProArgLeuGlnGluGlySerLeuSerSerSerLysAlaSer 1580
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QY 1581 GlnAspArgLysLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrVal 1600
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QY 1601 ProGluHisHisProHisProIleSerProTyArgGluHisLeuLeuArgGlyValSerGly 1620
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QY 1621 ValAspLeuTyArgSerHisIleProLeuAlaPheAspProThrSerIleProArgGly 1640
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QY 1641 IleProLeuAspAlaAlaAlaTyTyLeuProArgHisLeuAlaProAsnProThr 1660
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QY 1661 TyrProHisLeuTyProProTyTyLeuIleArgGlyTyProAspThrAlaAlaLeuGlu 1680
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QY 1681 AsnArgGlnThrIleIleAsnAspTyIleThrSerGlnGlnMetHisHisAsnThrAla 1700
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QY 1701 ThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSerProArgGluSerSerLeu 1720
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QY 1721 AlaLeuAsnTyAlaAlaGlyProArgGlyIleIleAspLeuSerGlnValProHisLeu 1740
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QY 1741 ProValLeuValProProThrProGlyThrProAlaThrAlaMetAspArgLeuAlaTy 1760
Db 5221 CCTGTCTGTGCCCCCGACACAGGCAACCCAGGACCGCGCATGCGCTTGCCTAC 5280
QY 1761 LeuProThrAlaProGlnProPheSerSerArgHisSerSerSerProLeuSerProGly 1780
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QY 1781 GlyProThrHisLeuThrLysProThrThrThrSerSerSerGluArgGluArgAspArg 1800
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QY 1801 AspArgGluArgAspArgAspArgGluArgGluLysSerIleLeuThrSerThrThrThr 1820
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QY 1821 ValGluHisAlaProIleTyrArgProGlyThrGluGlnSerSerGlySerSerGlySer 1840
Db 5461 GTGAGGACCGACCCATCTGGAGACCTGGTACAGACAGCAGCAGCGGACGAGCGGCGAG 5520
QY 1841 SerGlyGlyGlyGlySerSerArgProAlaSerHisSerHisAlaHisGlnHis 1860
Db 5521 AGCGCGCGGCTGGGCGCAGCAGCAGCGCGCGCTCCACCTCCCACTCCCACTCCACGAG 5580
QY 1861 SerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProSerValLeuHisAsn 1880
Db 5581 TCGCCCCATCTCCCTCGGACCCAGGATGCCCTCCAGCAGAGACCCAGTGTGCTTCAAC 5640

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QY 1881 ThrGlyMetLysGlyIleIleThrAlaValGluProSerLysProThrValLeuArgSer 1900
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QY 1901 ThrSerThrSerSerProValArgProAlaAlaThrPheProProAlaThrHisCysPro 1920
DB 5701 ACCTCCACCTCTCAGCCGTTCCGCCAGCTGCCACATTCACCTGCCACCACTGCCCA 5760
QY 1921 LeuGlyGlyThrLeuAspGlyValTyrProThrLeuMetGluProValLeuLeuProLys 1940
DB 5761 CTGGGGGGACCTTCGATGGGGTCTACCTTACCCTCATGGAGCCCGTCTTGTCTGCCCAAG 5820
QY 1941 GluAlaProArgValAlaAlaArgProGluArgProArgAlaAlaAspThrGlyHisAlaPheLeu 1960
DB 5821 GAGGCCCCCGGGTGGCCCGCCAGAGCGGCCCGGAGCAGACACCGGCCCATGCTTCTCTC 5880
QY 1961 AlaLysProProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGlu 1980
DB 5881 GCCAAGCCCCCAGCCCGCTCCGGGCTGGAGCCCGCTCTCTCCCCAGCAAGGGCTCGGAG 5940
QY 1981 ProArgProLeuValProProValSerGlyHisAlaThrIleAlaArgThrProAlaLys 2000
DB 5941 CCCGGGCCCCCTAGTGCCTCTCTGTCTCTGGCCAGCCACCATCGCCCGCACCTTGGCAAG 6000
QY 2001 AsnLeuAlaProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAsp 2020
DB 6001 AACTCGCACCTCACACGCGCAGCCCGGACCCCGCGGCCACCTGCTCGGCTCGGAC 6060
QY 2021 ProHisArgGlyLysThrGlnSerLysProPheSerIleGlnGluLeuLeuArgSer 2040
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QY 2041 LeuGlyTyrHisGlySerSerTyrSerProGluGlyValGluProValSerProValSer 2060
DB 6121 CTGGGTATACACCGCAGCAGCTACAGCCCGGAGGGGTGGAGCCCGTACGCTTGTGAGC 6180
QY 2061 SerProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluLeuAspLysSer 2080
DB 6181 TCACCCAGTCTGACCCACGACAGAGGGGCTCCCCAGACACCTGGAGAGCTCGACAGAGC 6240
QY 2081 HisLeuGluGlyGluLeuArgProLysGlnProGlyProValLysLeuGlyGlyGluAla 2100
DB 6241 CACCTGGAGGGGAGCTGCGGCCCAAGCAGCAGCCCGCTGGAAGCTTGGCGGGAGGCC 6300
QY 2101 AlaHisLeuProHisLeuArgProLeuProGluSerGlnProSerSerSerProLeuLeu 2120
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QY 2121 GlnThrAlaProGlyValLysGlyHisGlnArgValValThrLeuAlaGlnHisIleSer 2140
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QY 2141 GluValIleThrGlnAspTyrThrArgHisIleProGlnGlnLeuSerAlaProLeuPro 2160
DB 6421 GAGGTATCATCAGAGGACTACCCCGGCACACCCAGCAGCTCAGCGCACCCCTGCC 6480
QY 2161 AlaProLeuTyrSerPheProGlyAlaSerCysProValLeuAspLeuArgProPro 2180
DB 6481 GCCCCCTCTACTCTCTCTCGGGCCAGCTGCCCCGCTCTGGACCTCCCGCGCCACCC 6540
QY 2181 SerAspLeuTyrLeuProProProAspHisGlyAlaProAlaArgGlySerProHisSer 2200
DB 6541 AGTGACCTTACTCTCCCGCCCCCGGACCATGGTGCCCGCGCGCTGGCTCCCCCAGC 6600
QY 2201 GluGlyLysArgSerProGluProAsnLysThrSerValLeuGlyGlyGluAsp 2220
DB 6601 GAAGGGGCAAGAGTCTCCAGAGCCCAACAAGACGTCGGTCTTGGGTGGTGGAGGAC 6660
QY 2221 GlyIleGluProValSerProProGluGlyMetThrGluProGlyHisSerArgSerAla 2240
DB 6661 GGTATTGAACCTGTGTCCCAACCGAGGGCATGACGAGCCAGGCGCACTCCCGAGTGTCT 6720
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QY 2241 ValTyrProLeuLeuTyrArgAspGlyGluGlnThrGluProSerArgMetGlySerLys 2260
DB 6721 GTGTACCCGCTGTGTACCGGATGGGAAACAGACGAGCCAGGATGGGCTCCAAG 6780
QY 2261 SerProGlyAsnThrSerGlnProProAlaPheSerLysLeuThrGluSerAsnSer 2280
DB 6781 TCTCCAGGCAACACCAAGCCAGCCGCGAGCTTCTTACGCAAGCTGACGAGACACTCC 6840
QY 2281 AlaMetValLysSerLysGlnGluIleAsnLysLysLeuAsnThrHisAsnArgAsn 2300
DB 6841 GCCATGGTCAAGTCCAAGAGCAAGAGATCAACAAGAAGCTGAACACCCACCGGAAT 6900
QY 2301 GluProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAlaIleThr 2320
DB 6901 GAGCCTGAATACATATATCAGCCAGCCTGGGACGAGATCTTCAATATATGCGGCATCACC 6960
QY 2321 GlyThrGlyLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMet 2340
DB 6961 GGAAACAGGCTTATGACCTATAGAAGCCAGCGGTGAGGAACATGCCAGCACCAATG 7020
QY 2341 GlyLeuGluAlaIleIleArgLysAlaLeuMetGlyLysTyrAspGlnTyrGluGlySer 2360
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QY 2381 MetProIleThrAlaAlaAspGlyArgSerAspHisThrLeuThrSerProGlyGlyGly 2400
DB 7141 ATCCCATTAACCCGCTGCTGACGACGGAGTGACACACTCACCTCGCAGGTGGCGGC 7200
QY 2401 GlyLysAlaLysValSerGlyArgProSerSerArgLysAlaLysSerProAlaProGly 2420
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QY 2421 LeuAlaSerGlyAspArgProProSerValSerSerValHisSerGluGlyAspCysAsn 2440
DB 7261 CTGGCATCTGGGACCGGCCACCTCTGTCTCTCTCAGTGCACCTCGAGGGAGACTGCAAC 7320
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DB 7321 CGCGGACGCGCTCAACACCCGCTGTGGAGGACAGGCCCTCGTCCGACAGGTTCACG 7380
QY 2461 ProPheProTyrAsnProLeuIleMetArgLeuGlnAlaGlyValMetAlaSerProPro 2480
DB 7381 CCATTCCCTTACAAACCCCTGATCATGCGGCTGCAGGGGGTGTCTATGGCTTCCCAACC 7440
QY 2481 ProProGlyLeuProAlaGlySerGlyProLeuAlaGlyProHisIleAlaTyrAspGlu 2500
DB 7441 CCACCGGCTCCCGCGGCGCAGCGGCCCTCGCTGGCCCCCACCACCGCTGGGAGGAG 7500
QY 2501 GluProLysProLeuLeuCysSerGlnTyrGluThrLeuSerAspSerGlu 2517
DB 7501 GAGCCCAAGCACTGCTCTCTCGAGTACGAGACACTCTCCGACAGCGAG 7551
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RESULT 2

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US-10-174-014-11
; Sequence 11, Application US/10174014
; Publication No. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PFS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 11
; LENGTH: 8561
; TYPE: DNA
; ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: CDS
LOCATION: (2)...(7555)
US-10-174-014-11

Alignment Scores:

Pred. No.: 0 Length: 8561
Score: 13215.00 Matches: 2517
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-522-753-5 (1-2517) x US-10-174-014-11 (1-8561)

QY 1 MetSerGlySerThrGlnLeuValAlaGlnThrTrpArgAlaThrGluProArgTyrPro 20
DB 2 ATGTGGGGCTCCACACAGCTTGTGGCACAGACGTGGAGGGCCACTGAGCCCGCTACCCG 61
QY 21 ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
DB 62 CCCACAGCCCTTTCCTACCCAGTGCAGATGCCCGGAGGCACACGAGCGTGGGGCTCCTG 121
QY 41 GluTyrGlnHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleIleGln 60
DB 122 GAGTACCAGCACCACTCCCGCGACTATGCTCCACCTGTCGCGGGCTCCATCATCCAG 181
QY 61 ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
DB 182 CCCACGGGGAGGGCCCTCCCTGCTGCTGAGTTCAGCCCGGGAATGAACGGTCCCAG 241
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
DB 242 GAGCTCCACTGGCGGCAGAGTCCCACTCATCTGCCCCGAGCTGGGGAAGTCAAGATG 301
QY 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
DB 302 GAGTTCAATGAAGAGAGCCCTCGCTAGAGCTGCTGCTGACCCCTGCTGCGACCG 361
QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
DB 362 TCACCCCTGCTGGCCACAGGCCAGCTGCGGAGTCTGAAGACCTCAACAGGACCGTAGC 421
QY 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
DB 422 CTGACGGGCAAGCTGNAACGGGTGTCTCCCCCAGCCCCCGCACACTGACCTGAGCTG 481
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAsnMetAspArgValAsp 180
DB 482 GAGCTGTCGCGCCACGGCTGTCCAGGAGAGCTGATCCAGAACATGGACCGCGTGGAC 541
QY 181 ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGlnLeu 200
DB 542 CGAGAGATCACTACCTGTAGACGACAGATCTCTAAGCTGAAGAGAGAGCAGCAACAGCTG 601
QY 201 GluGluGluAlaAlaLysProGluProGluLysProValSerProProIleGlu 220
DB 602 GAGGAGAGGCTGCCAAGCGCCCGGAGCTGAGAGCCCGTGTACCGCGCCCATCGAG 661
QY 221 SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGluAla 240
DB 662 TCGAAGCAGCGACGCTGTGTGAGATCATCTACGACGAGAACCGGAAGGCTGAAGCT 721
QY 241 AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro 260
DB 722 GCACATCGAATCTTGAAGGCCCTGGGGCCCCAGGTGAGCTGCGCGTGTACACACGACCC 781
QY 261 SerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu 280
DB 782 TCCGACACCGCGGAGTATCATGAGACATCAAAATAAACACGCGGATGCGGAGAGAGCTA 841
QY 281 IleLeuTyrPheLysArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCysGln 300

DB 842 ATCTTGTTACTTCAAGAGGAGGAATCACGCTCGGAAACAATGGAAGCAGAGATTTCTGCCAG 901
QY 301 ArgTyrAspGlnLeuMetGluAlaLeuGluLysValGluArgIleGluAsnAspPro 320
DB 902 CGCTATGACCAGCTCATGGAGGCTTGGAAAAAAGGTGGAGCGCATCGAAAAACAACCCG 961
QY 321 ArgArgArgAlaLysGluSerLysValArgGluTyrTyrGluLysGlnPheProGluIle 340
DB 962 CGCCGCGGGCCAAAGGAGAGCAGAGTGGCGAGTACTACGAAAGCAGTTCCTCGAGATC 1021
QY 341 ArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgValGlyGlnArgGlySerGly 360
DB 1022 CGCAAGCAGCGCGAGCTGCAGAGCGCATGCGAGAGGAGGTCGCGCCAGCGCGGCGAGTGG 1081
QY 361 LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleLeuSerGlyLeuSer 380
DB 1082 CTGTCTCATGTGCGCCCGCCGACGAGCAGAGTGTGAGATCATCATGATGCGCTCTCA 1141
QY 381 GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyr 400
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QY 401 AspAlaAspGlnGlnArgIleLysPheIleAsnMetAsnGlyLeuMetAlaAspProMet 420
DB 1202 GAGCTGACCCAGCAGCGGCATCAAGTTTCATCAACATGAACGGGCTTATGGCCGACCCATG 1261
QY 421 LysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluLysGluThrPhe 440
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QY 481 SerLeuValArgArgSerTyrArgArgGlyLysSerGlnGlnGlnGlnGlnGln 500
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QY 521 AspGluLysGluLysGluLysGluAlaGluLysGluGluLysProGluValGluAsn 540
DB 1562 GATGAGAGGAGAAAGGAGGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1621
QY 541 AspLysGluAspLeuLysGluLysThrAspAspThrSerGlyGluAspAsnAspGlu 560
DB 1622 GACAGGAGAGCTCTCTCAAGGAGAGAGCAGACGACCTCAGGAGGAGGAGCAGCAG 1681
QY 561 LysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgArgLysGly 580
DB 1682 AAGGAGCTGTGGCTTCCAAAGGCCCAAACTGCCAAAGCAGCAGGAGAGCAGCAGGAG 1741
QY 581 ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGluAlaIleThrProGlnGln 600
DB 1742 CGCATCACCGCTCAATGTGCTAATGAGGCAACAGCAGGAGGAGGAGGAGGAGGAGGAG 1801
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DB 1802 AGCGCGAGCTGGCTTCCATGGAGCTGAATGAGAGTTCCTGCTGGACAGAGAGAGATG 1861
QY 621 GluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTrpSerAlaIleAlaArgMet 640
DB 1862 GAAACAGCAACCAAGAGTCTCTGGNAACAGCGCCGCACTGGTTCGGCCATCGCCCGATG 1921
QY 641 ValGlySerLysThrValSerGlnCysLysAsnPheTyrPheAsnTyrLysLysArgGln 660
DB 1922 GTGGGCTCCAAGACTGTGTGCGAGTGTAAAGAACTTCTACTTCAACTACAAGAGAGGAG 1981

QY	661	AsnLeuAspGluIleLeuGlnGlnHisLysLeuLysMetGluLysGluArgAsnAlaArg	680
Db	1982	AACCTCGATGAGATCTTGCAGCAGCACAAGCTCAAGATGAGAGAGAGAGCGCGG	2041
QY	681	ArgLysLysLysAlaProAlaAlaLaserGluGluAlaAlaPheProValVal	700
Db	2042	AGGAAGAAGAAGAAAGCGCGCGCGCGCGAGGAGGCTGCATTCGCGCGCGTGGTG	2101
QY	701	GluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu	720
Db	2102	GAGGATGAGGAGATGAGGCGTCCGGCGTGAGCGGAAATGAGGAGAGATGGTGGAGGAG	2161
QY	721	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740
Db	2162	GCTGAAGCCTTACATGCTCTGGGAATGAGTGCACAGAGGGGAATGTCAGTGGCCAGCC	2221
QY	741	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaAlaLys	760
Db	2222	ACTGTCAACAACAGCTCAGACACGAGAGATCCCTCTCTCTCACACTGAGGCGGCAAG	2281
QY	761	AspThrGlyGlnAsnGlyProLysProProAlaThrLeuGlyAlaAspGlyProProPro	780
Db	2282	GACACAGGGGAGAATGGGCGCAAGCCCCAGCCAGCCCTGGGCGCGGAGCGGCCACCCCCA	2341
QY	781	GlyProProThrProProArgArgThrSerArgAlaProIleGluProThrProAlaSer	800
Db	2342	GGCCCAACCCACCCACGAGGAGACATCCCGGCGCCCCATTGAGCCACCCCGGCTCT	2401
QY	801	GluAlaThrGlyAlaProThrProProAlaProProSerProSerAlaProProPro	820
Db	2402	GAAGCACCGAGCGCCCTACGCGCCCAACACGAGCAGCCCGCCCTCTGCACTCTCTCT	2461
QY	821	ValValProLysGluGluLysGluGluThrAlaAlaAlaProValGluGluGly	840
Db	2462	GTGGTCCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2521
QY	841	GluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThrGlyLysAlaGluGlu	860
Db	2522	GAGGAGCAGAAGCCCCCGCGCTGAGGAGCTGGCAGTGACACAGGAGGCGGAGGAG	2581
QY	861	ProValLysSerGluCysThrGluGluAlaGluGluGluProAlaLysGlyLysAspAla	880
Db	2582	CCCGTCAAGAGCGAGTGCACGAGGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2641
QY	881	GluAlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysLysGluGlyGlySer	900
Db	2642	GAGGCCGCTGAGGCCACCGCGCGAGGCGGCGCTCAAGGCAGAGAGAGAGGAGGCGGAGC	2701
QY	901	GlyArgAlaThrThrAlaLysSerSerGlyValProGlnAspSerAspSerAlaThr	920
Db	2702	GGCAGGGCCACCACTGCCAAGAGCTCGGGCGCCCCCGAGGAGGAGGAGGAGGAGGAG	2761
QY	921	CysSerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPro	940
Db	2762	TGCAGTGCACAGCGAGTGGATGAGCGCGCGGCGGCGGAGGAGGAGGAGGAGGAGGAG	2821
QY	941	ArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGlnLysPro	960
Db	2822	AGGCCAGCGCTCTCTCAACCCGACTGGCGGACCCCCGGGCGCAATGCCTCACCCAGAGCCA	2881
QY	961	LeuAspLeuLysGlnLeuLysGlnArgAlaAlaIleProProIleGlnValThrLys	980
Db	2882	CTGGACCTGAAGCAGCTGAAGCAGCGAGCGGCTGCCATCCCCCGCATCCAGGTCACCAA	2941
QY	981	ValHisGluProProArgGluAspAlaAlaProThrLysProAlaProProPro	1000
Db	2942	GTCCATGAGCCCCCGGAGGAGCGAGCTCCCAACCAAGCCAGCTCCCGGAGGAGGAGGAG	3001
QY	1001	ProProGlnAsnLeuGlnProGluSerAspAlaProGlnGlnProGlySerSerProArg	1020
Db	3002	CCACCGCAAAACCTGACGCGGAGAGCGAGCGCCCTCAGCAGCGCTGGCAGCAGCGCCCGG	3061

QY	1021	GlyLysSerArgSerProAlaProProAlaAspLysGluAlaPheAlaAlaGluAlaGln	1040
Db	3062	GGCAAGAGCAGAGAGCGCGCACCCCGCGCCACAAAGAGGCGCTTCGAGCGGAGGCGCAG	3121
QY	1041	LysLeuProGlyAspProProCysTyrThrSerGlyLeuProPheProValProProArg	1060
Db	3122	AGCTCCCTGGGAGACCCCTTGTGGACTTCGGGCTGCGCTTCCTCCCGGCGCCCGCGT	3181
QY	1061	GluValIleLysAlaSerProHisAlaProAspProSerAlaPheSerTyrAlaProPro	1080
Db	3182	GAGTGATCAAGGCTCCCGCATGCGCGACCCCTCAGCCTTCTCTACGCTCCACCT	3241
QY	1081	GlyHisProLeuProLeuGlyLeuHisAspThrAlaArgProValLeuProArgProPro	1100
Db	3242	GGTCACCCACTGCGCTGGGCTCCATGACACTGCGCGCGCGCTCTCTCGCGCGCCACCC	3301
QY	1101	ThrLysSerAsnProProProLeuIleSerSerAlaLysHisProSerValLeuGluArg	1120
Db	3302	ACCATCTCAACCGCGCTCCCTCATCTCTGCGCAAGCACCCAGCGCTCTCGAGAGG	3361
QY	1121	GlnIleGlyAlaIleSerGlnGlyMetSerValGlnLeuHisValProTyrSerGluHis	1140
Db	3362	CAATAGTGCCATCTCCNAGGAAATGTGGTCCAGCTCCAGCTCCGCTACTCAGAGCAT	3421
QY	1141	AlaLysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspProLysLys	1160
Db	3422	GCCAAAGCGCGCGTGGCTGTGACCATGGGGCTGCGCTGCCATGAGACCCCAAAAG	3481
QY	1161	LeuAlaProPheSerGlyValLysGlnGlnLeuSerProArgGlyGlnAlaGlyPro	1180
Db	3482	CTGGCACCTTTCAGCGGAGTGAAGCAGGAGCAGCTGTCCCAAGGCGGCGGCTGGGCCA	3541
QY	1181	ProGluSerLeuGlyValProThrAlaGlnGluAlaSerValLeuArgGlyThrAlaLeu	1200
Db	3542	CCGAGAGCTGGGGTGCCACAGCCAGAGGCGCTCCGTGTGAGAGGAGCAGCTCTG	3601
QY	1201	GlySerValProGlyGlySerIleThrLysGlyLysGlyLysProSerThrArgValProSerAsp	1220
Db	3602	GGCTCAGTTCGCGCGGAGCATCAGCAAGGCAATTCAGCAGCACACGGTGCCTCGGAC	3661
QY	1221	SerAlaIleThrThrArgGlySerIleThrHisGlyThrProAlaAspValLeuTyrLys	1240
Db	3662	AGCGCATCACATACCGCGCTCCATCCAGCGCAGCGCAGCTGACGTCTGTGTACAG	3721
QY	1241	GlyThrIleThrArgIleIleGlyGluAspSerProSerArgLeuAspArgGlyArgGlu	1260
Db	3722	GGCACCATCACAGGATCATCGCGAGGAGCAGCCCGAGTCCGTTCGACCGCGCGGAG	3781
QY	1261	AspSerLeuProLysGlyHisValIleTyrGluGlyLysLysGlyHisValLeuSerTyr	1280
Db	3782	GACAGCTGCGCAAGGCGCACGTCATCTACGAAGGCAAGAGGCGCACGCTTGTCTCTAT	3841
QY	1281	GluGlyGlyMetSerValThrGlnCysSerLysGluAspGlyArgSerSerSerGlyPro	1300
Db	3842	GAGGGTGGCATGTCTGTGACCCAGTCTCCAGGAGACCGCAGAGCAGCTCAGGACCC	3901
QY	1301	ProHisGluThrAlaAlaProLysArgThrTyrAspMetMetGluGlyArgValGlyArg	1320
Db	3902	CCCCATGAGAGCGCGCGCCCAAGCGCATATGACATGATGAGAGGCGCGCTGGGAGA	3961
QY	1321	AlaIleSerSerAlaSerIleGluGlyLeuMetGlyArgAlaIleProProGluArgHis	1340
Db	3962	GCCATCTCTCAGCAGCATCGAAGGTCTCATGGCGCTGCCATCCCGCGGAGGAGCAGC	4021
QY	1341	SerProHisLysLeuLysGlnHisIleArgGlySerIleThrGlnGlyIlePro	1360
Db	4022	AGCCCCCACCTCAAGAGCAGCAGCACCATCCGCGGGTCCATCACACAGGAGATCCCT	4081
QY	1361	ArgSerTyrValGluAlaGlnGluAspTyrLeuArgGluAlaLysLeuLeuLysArg	1380
Db	4082	CGTCTCTAGTGGAGGACAGGAGGAGTACTCGGTCCGAGGAGGAGGAGGAGGAGGAGG	4141
QY	1381	GluGlyThrProProProProProSerArgAspLeuThrGluAlaTyrLysThrGln	1400

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4142 GAGGCGACGCTCCGCGCCACCGCCCTCAGCGGACCTCAGGAGCCCTACAGAGCGCAG 4201
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1401 AlaLeuGlyProLeuLysLeuLysProAlaHisGluGlyLeuValAlaThrValLysGlu 1420
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4202 GCCCTGGGCCCTTGAAGCTGAAGCCCGGCCCATAGGGCTGGTGGCCACGGTGAAGAG 4261
QY
1421 AlaGlyArgSerIleHisGluIleProArgGluGluLeuArgHisThrProGluLeuPro 1440
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4262 GCGGCGCGCTCCATCATGATGATCCCGCGAGAGCTCGGCGACACGCGCCGAGCTGCC 4321
QY
1441 LeuAlaProArgProLeuLysGluLysIleThrClnGlyThrProLeuLysTyrAsp 1460
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4322 CTGCGCCCGCGCGCTCAAGAGGGCTCCATCAGCAGGGCACCCCGCTCAAGTACGAC 4381
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1461 ThrGlyAlaSerThrThrGlySerLysLysHisAspValArgSerLeuIleGlySerPro 1480
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1641 IleProLeuAspAlaAlaAlaTyrTyrLeuProArgHisLeuAlaProAsnProThr 1660
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1741 ProValLeuValProProThrProGlyThrProAlaThrAlaMetAspArgLeuAlaTyr 1760
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1801 AspArgGluArgAspArgAspArgGluArgLysSerIleLeuThrSerThrThrThr 1820
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5462 GTGAGACGACGACCATCTGAGACCTGGTACAGAGCAGAGCGGCGAGCAGCGGACG 5521
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Db
5522 ACGCGCGGGGTGGGGGAGCAGCAGCGCCCGCTCCCACTCCCATGCCACCAACGAGC 5581
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1861 SerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProSerValLeuHisAsn 1880
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5822 GAGGCCCCCGGGTGGCCCGGCGAGCGGCCCCGAGCAGACACCGGCTTCCTCTCTC 5881
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1961 AlaLysProProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGlu 1980
Db
5882 GCCAAGCCCCAGCCCGCTCCGGGTGGAGCGCGCTCTCCCGCAGCAAGGGCTCGGAG 5941
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5942 CCGCGCCCTTAGTGCTCTGTCTGTGCCACGCCACCATCGCCGCGACCCCTTGGGAG 6001
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Db
6002 AACCTCGACCTCACCAACCGGACCGCGCGGCGGCGGCTGCTCGCTCGGCTCGGAC 6061
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161 QY GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAsnMetAspArgValAsp 180
162 DB |
596 DB GAGCTGGTCCGCGCACGGCTGTCCAGGAGGAGCTCATCAGAACATGACCGCGTGGAC 655
181 QY ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnLeu 200
182 DB |
656 DB CGAGAGATCACCATGTGTAGCAGCAGAGATCTCTTAAGCTGAAGAAGACAGCAACAGCTG 715
201 QY GluGluGluAlaLysProGluProGluLysProValSerProProIleGlu 220
202 DB |
716 DB GAGGAGGAGCTGCCAAGCGCCGCGAGCTGTGAAGCCCGTGTACCGCGCCCATCGAG 775
221 QY SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGluAla 240
222 DB |
776 DB TCGAAGCACCGCAGCTGTGTGCAGATCATACGACGAGAACCGGAAGAGCTGAAGCT 835
241 QY AlaHisArgIleLeuGluGluLysGluGluValGlnValGluLeuProTyrAsnGlnPro 260
242 DB |
836 DB GCACATCGGATTCTGAAGCGCTGGGGCCCGCAGGTGGAGCTGCGCTGTACAAACAGCCG 895
261 QY SerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu 280
262 DB |
896 DB TCCGACACCGCGCAGTATCATGAGACATCAAAATAAACCGCGCATGCGGAAGAGCTA 955
281 QY IleLeuTyrPheLysArgArgAsnHisAlaArgLysGlnTyrLysPheCysGln 300
282 DB |
956 DB ATCTTGATCTTCAAGAGGAGGAATCAGCTCGGAACATGGGAGCAGAGTTCTGCCAG 1015
301 QY ArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAsnPro 320
302 DB |
1016 DB CGCTATGACCGAGCTCATGGAGGCTCGGAGAAAGGTGGAGCGCATCGAAGAACACCCG 1075
321 QY ArgArgArgAlaLysGluSerLysValArgGluTyrTyrGluLysGlnPheProGluIle 340
322 DB |
1076 DB CGCGCGCGCGCAAGAGAGCAAGGTGCGAGTACTACGAGAAGCAGTTCCCTGAGATC 1135
341 QY ArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgValGlyGlnArgGlySerGly 360
342 DB |
1136 DB CGCAAGCAGCGCAGCTGCAGAGCGCATGCAGACGAGGTGGCGCAGCGGGCAGTGGG 1195
361 QY LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeuSer 380
362 DB |
1196 DB CTGTCCATGTCCGCGCGCCGACGAGCAGCAGGTGTTCAGAGATCATCGATGGCCCTCTCA 1255
381 QY GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyr 400
382 DB |
1256 DB GACGAGAGAACCTGGAGAAGCAGATGCGCCAGCTGGCCGTGATCCCGCCCATGCTGTAC 1315
401 QY AspAlaAspGlnGlnArgIleLysPheIleAsnMetAsnGlyLeuMetAlaAspProMet 420
402 DB |
1316 DB GACGCTGACGACGAGCGCATCAAGTTTCATCAACATGAACGGGCTTATGGCCGACCCCATG 1375
421 QY LysValTyrLysAspArgGlnValMetAsnMetTyrSerGluGlnGluLysGluThrPhe 440
422 DB |
1376 DB AAGGTGTACAAAGACCGCCAGGTGCATGAACATGTGGAGTGAGCAGGAGAAGGAGACCTTC 1435
441 QY ArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIleAlaSerPheLeuGluArg 460
442 DB |
1436 DB CGGGAGAAGTTTCATGAGCATCCAGAACTTTGGCCGTGATCCGATCATTTCTCTGGAGAGG 1495
461 QY LysThrValAlaGluCysValLeuTyrTyrTyrLeuThrLysLysAsnGluAsnTyrLys 480
462 DB |
1496 DB AAGACAGTGGCTGAGTGGCTCTCTATTACTACTGACTAAGAAAGATGAGAACTATAG 1555
481 QY SerLeuValArgArgSerTyrArgArgGlyLysSerGlnGlnGlnGlnGln 500
482 DB |
1556 DB AGCCTGTGAGACGAGCTATCGCGCGCGGCAAGAGCCAGCAGCAGCAACAAACAGCAGCAG 1615
501 QY GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnProMetProArgSerGlnGluLys 520
502 DB |
1616 DB CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1675

521 QY AspGluLysGluLysGluLysGluAlaGluLysGluGluLysProGluValGluAsn 540
522 DB |
1676 DB GATGAGAAGGAGAAAGGAGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1735
541 QY AspLysGluAspLeuLysGluLysThrAspAspThrSerGlyGluAspAspGlu 560
542 DB |
1736 DB GACAAAGGAGAGCTCTCTCAAGGAGAGACAGACGACACCTCTCAGGGGAGGACCAACGACGAG 1795
561 QY LysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgArgLysGly 580
562 DB |
1796 DB AAGGAGGCTGTGGCTCCAAAGCGCCGCAAACTGCCAACAGCAGCAGGAGAGCGCAAGGC 1855
581 QY ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGluAlaIleThrProGlnGln 600
582 DB |
1856 DB CGCATCACCGCTCAATGGCTAATGAGGCAACAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1915
601 QY SerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTyrThrGluGluMet 620
602 DB |
1916 DB AGCGCGAGCTGGCTCCATGGAGCTGAATGAGAGTTCTCGCTGGACAGAAAGAAATG 1975
621 QY GluThrAlaLysLysGlyLeuLeuHisGlyArgAsnTyrSerAlaIleAlaArgMet 640
622 DB |
1976 DB GAACACGACCAAGAGGTCTCTGGACACAGCGCCGCACTGGTGGCCCATCGCCCGGATG 2035
641 QY ValGlySerLysThrValSerGlnCysLysAsnPheTyrPheAsnTyrLysLysArgGln 660
642 DB |
2036 DB GTGGGCTCAAGACTGTGTGCGAGTGTAAAGAACTTCTACTTCAACTACAAGAGAGGCGAG 2095
661 QY AsnLeuAspGluIleLeuGlnGlnHisLysLeuLysMetGluLysGluArgAsnAlaArg 680
662 DB |
2096 DB AACCTCGATGAGATCTTGACGAGCACAAGCTGAAGATGGAGAGGAGGAGGAGGAGGAGGAG 2155
681 QY ArgLysLysLysAlaProAlaAlaSerGluGluAlaAlaPheProValVal 700
682 DB |
2156 DB AGAAGAAAGAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2215
701 QY GluAspGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu 720
702 DB |
2216 DB GAGGATGAGGAGATGGAGGCGTGGGCGGTGAGCGGAATGAGGAGGAGATGGTGGAGGAG 2275
721 QY AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyCysSerGlyProAla 740
722 DB |
2276 DB GCTGAAGCTTACATGCCCTCGGAATGAGGTGCCAGAGGGAATGCGAGTGGCCCGCGCG 2335
741 QY ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaLys 760
742 DB |
2336 DB ACTGTCAACACAGCTCAGACCGAGAGCATCCCTCTCTCCTCAGCTGAGGCGCGCAAG 2395
761 QY AspThrGlyGlnAsnGlyProLysProAlaThrLeuGlyAlaAspGlyProProPro 780
762 DB |
2396 DB GACACAGGCGAATGGGCGCAAGCGCCGAGCCACCTGGGCGCGCGCGCGCGCGCGCGCGCGCG 2455
781 QY GlyProThrProPro-ArgArgThrSerArgAlaProIleGluProThrProAlaSe 800
782 DB |
2456 DB GGCGCACCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2514
800 QY rGluAlaThrGlyAlaProThrProProAlaProProSerProSerAlaProProPr 820
801 DB |
2515 DB TGNAGCCACCGGAGCGCCCTACGCCCCCAGCAGCAGCCCCCATCGCCCTCTGCTCCTCTCC 2574
820 QY oValValProLysGluGluLysGluGluThrAlaAlaProProValGluGlu 840
821 DB |
2575 DB TGTGTGTCCTCAAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2634
840 QY yGluGluGlnLysProProAlaAlaGluLeuAlaValAspThrGlyLysAlaGlu 860
841 DB |
2635 DB GGAGGAGCAGAAAGCCCCCGCGCTGAGGAGCTGGCAGTGGACACAGGAAAGGCCGAGGA 2694
860 QY uProValLysSerGluCysThrGluGluAlaGluGluGlyProAlaLysGlyLysAspAl 880
861 DB |
2695 DB GCCCGTCAAGCGCAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2754
880 QY aGluAlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysGlyGlyGly 900

Db 2755 GGAGCCGCTGAGGCCACGCGCGAGGGGGCGCTCAAGGCGACAGAAAGAGGGCGCGAG 2814
Qy 900 rGlyArgAlaThrThrAlaLysSerSerGlyAlaProGlnAspSerAspSerAlaLys 920
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Qy 920 rCySerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPr 940
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Db 2995 ACTGGACCTGAGCAGCTGAAGCAGCAGCGGGTGCATCCCCCCTCCAGGTACCAA 3054
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Qy 1100 oThrIleSerAsnProProProLeuLysSerAlaLysHisProSerValLeuGluAr 1120
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Qy 1140 sAlaLysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspProLysLy 1160
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Qy 1240 sGlyThrIleThrArgIleIleGlyGluAspSerProSerArgLeuAspArgGlyArgGl 1260

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Qy 1340 sSerProHisHisLeuLysGlnHisHisIleArgGlySerIleThrGlnGlyIlePr 1360
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Qy 1360 oArgSerTyrValGluAlaGlnGluAspTyrLeuArgArgGluAlaLysLeuLeuLysAr 1380
Db 4195 TCGTCTCTACGTGGAGGCAAGAGGACTACCTGCGTCCGGGAGGCGCAAGCTCTAAAGCG 4254
Qy 1380 sGluGlyThrProProProProProSerArgAspLeuThrGluAlaTyrLysThrGl 1400
Db 4255 GGAAGGCAAGCTTCCCGCCCCCAGCCCTCAGCGGACCTGACCGAGGCTTACAGAGCGCA 4314
Qy 1400 nAlaLeuGlyProLeuLysLeuLysProAlaHisGluGlyLeuValAlaThrValLysGl 1420
Db 4315 GGGCTTGGGCCCCCTGAAGCTGAAGCGCGCCCATGAGGGCTGTGTGSCCAGCGTGAAGGA 4374
Qy 1420 uAlaGlyArgSerIleHisGluIleProArgGluGluLeuArgHisThrProGluLeuPr 1440
Db 4375 GCGGGCGCTTCATCATCATGAGATCCCGCGGAGGAGCTGCGGACACACGCGCGAGCTGCC 4434
Qy 1440 oLeuAlaProArgProLeuLysGluGlySerIleThrGlnGlyThrProLeuLysTyrAs 1460
Db 4435 CTTGGCCCCCGGCGCGCTCAAGAGGGCTCCATCAGCGGGGACCCCGCTCAAGTACGA 4494
Qy 1460 pThrGlyAlaSerThrThrGlySerLysLysHisAspValArgSerLeuIleGlySerPr 1480
Db 4495 CACCGGGGCTCCACCTGGCTCCAAAAGACAGAGTACGCTCCCTCATCGGAGCCC 4554
Qy 1480 oGlyArgThrPheProProValHisProLeuAspValMetAlaAspAlaAlaLeuGl 1500
Db 4555 CGGCCGAGCGTTCCCAACCGGTGCACCGCTGGATGTGATGGCGAGCGCCGCGACTGGA 4614
Qy 1500 uArgAlaCysTyrGluGluSerLeuLysSerArgProGlyThrAlaSerSerSerGlyGl 1520
Db 4615 AGTGTCTGCTACGAGGAGCGCTGAAGAGCGCGGACCGGAGCGCGAGCTCGGGGG 4674
Qy 1520 ySerIleAlaArgGlyAlaProValIleValProGluLeuGlyLysProArgGlnSerPr 1540
Db 4675 CTCCATTGCGGGCGGCGCCCGGTCAATTGTGCTGAGCTGGGCAAGCGCGGAGAGCCC 4734
Qy 1540 oLeuThrTyrGluAspHisGlyAlaProPheAlaGlyHisLeuProArgGlySerProVa 1560
Db 4735 CCTAACCTATGAGGACACAGGGGACCCCTTTGCGGCGCACCTCCACAGAGTTCCGCCGT 4794
Qy 1560 lThrMetArgGluProThrProArgLeuGlnGlySerLeuSerSerSerLysAlaSe 1580
Db 4795 GACCGCGGGAGCCACCGCGCTGAGGAGGCGAGCCTTCTGTCAGAGAGGCATC 4854
Qy 1580 rGlnAspArgLysLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrVa 1600
Db 4855 CAGGACCGAAGAGTGAAGCTGAGCGCTCTGTGATGCGCAGTCCCGCAGACACCGT 4914
Qy 1600 lProGluHisHisProHisProIleSerProTyrGluHisLeuLeuArgGlyValSerGl 1620
Db 4915 GCGCGAGCACCCACACCCCATCTCGCCCTATGAGCACCTGCTTTCGGGGCGGTGAGTGG 4974

QY 1620 yValAspLeuTyrArgSerHisIleProLeuAlaPheAspProThrSerIleProArgI 1640
DB 4975 CGTGGACCTGTATCGAGCCACATCCCTGGCTTCGACCCACCTCATACCCCGCG 5034
QY 1640 yIleProLeuAspAlaAlaAlaTyrTyrLeuProArgHisLeuAlaProAsnProTh 1660
DB 5035 CATCCCTCTGGACGACCGCTGCCTACTACCTGCCCGGACACCTGGCCCCCAACCCAC 5094
QY 1660 rTyrProHisLeuTyrProProTyrIleuIleArgGlyTyrProAspThrAlaAlaLeuGI 1680
DB 5095 CTACCCGCACTGTATCCCACTTACCTATCCCGGCTACCCCGACACCGCGCGCTGGA 5154
QY 1680 uAenArgGlnThrIleIleAsnAspTyrIleThrSerGlnGlnMetHisHisAsnThrAl 1700
DB 5155 GAACCGGCGAGACCATCATCATGACTATCATCACTCGAGCAGATGCACACACCGCGC 5214
QY 1700 aThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeuSerProArgGluSerSerLe 1720
DB 5215 CACCGCATGGCCCGACGAGCTGATATGCTGAGGGGCTCTCGCCCGGAGTCTCGCT 5274
QY 1720 uAlaLeuAsnTyrAlaAlaGlyProArgGlyIleIleAspLeuSerGlnValProHisLe 1740
DB 5275 GGCACCTCAACTACGCTGCGGGTCCCGAGGCATCATCGACCTGTGCCAAGTGCACACCT 5334
QY 1740 uProValLeuValProProThrProGlyThrProAlaThrAlaMetAspArgLeuAlaTy 1760
DB 5335 GCCTGTGCTGTGCCCCGACACCGAGCCACCCAGCCACCGCATCGACCGCTTCCTTA 5394
QY 1760 rLeuProThrAlaProGlnProPheSerSerArgHisSerSerSerProLeuSerProGI 1780
DB 5395 CTTCCCAACCGCGCCCGAGCCCTTCAGACGCGCCACAGCAGCTCCCACTCTCCCGAG 5454
QY 1780 yGlyProThrHisLeuThrIleProThrThrThrSerSerSerGluArgGluArgAspAr 1800
DB 5455 AGTGTCAACACACTTGACAAACCAACCAACCACTCGTCTCGTCCGAGCGGAGGAGACCG 5514
QY 1800 gAspArgGluArgAspArgGluArgGluLysSerIleLeuThrSerThrThrTh 1820
DB 5515 GGATCGAGAGCGGAGCGGATCGGAGCGGGGAAAGTCCATCTCATCGTCCACACGAC 5574
QY 1820 rValGluHisAlaProIleTrpArgProGlyThrGluGlnSerSerGlySerSerGlySe 1840
DB 5575 GGTGGAGCAGCACCCATCTGGAGACCTGGTACAGACGAGCAGCGCGGAGCAGCGCAG 5634
QY 1840 rSerGlyGlyGlyGlySerSerSerArgProAlaSerHisSerHisAlaHisGlnHi 1860
DB 5635 CAGCGCGGGGGTGGGGGCGAGCAGCGCCCGCTCCCACTCCCATGCCCCACACGCA 5694
QY 1860 sSerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProSerValLeuHisAs 1880
DB 5695 CTGCCCCATCTCCCTCGGACCCAGATGCCCTCCAGCAGAGACCCAGTGTGCTTCACAA 5754
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DB 5755 CACAGGCATGAAGGTATCATCACCGCTGTGGAGCGCAGCACGCCCATCGTCTGAGGTC 5814
QY 1900 rThrSerThrSerSerProValArgProAlaAlaThrPheProProAlaThrHisCysPr 1920
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QY 1920 oLeuGlyGlyThrLeuAspGlyValTyrProThrLeuMetGluProValLeuLeuProLy 1940
DB 5875 ACTGGGGCGCACCTCGATGGGTCTACCTTACCTCATGGAGCCGCTCTGTGCCCCAA 5934
QY 1940 sGluAlaProArgValAlaArgProGluArgProArgAlaAspThrGlyHisAlaPheLe 1960
DB 5935 GGAGGCCCCCGGCTCGCCCGGCGAGCGGCCCCGAGCAGACACCGGCCATCGCTTCCT 5994
QY 1960 uAlaLysProProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGI 1980
DB 5995 CGCCAAAGCCCCGAGCCGCTCCGGGCTGGAGCCCGCTCTCTCCCGCAGCAAGGGGCTCGGA 6054

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QY 2000 sAsnLeuAlaProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAs 2020
DB 6115 GAACCTCGACCTCACCGACCGCGGACCGCGCGGCGCACCTGCTGCTCGGCTCGGA 6174
QY 2020 pProHisArgGluLysThrGlnSerLysProPheSerIleGlnGluLeuGluLysArgSe 2040
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QY 2060 rSerProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGluLysAspLysSe 2080
DB 6295 CTCACCCAGTCTGACCCACGACAAAGGGGTCTCCCAAGCAGCCTTGAAGAGCTCGACAGAG 6354
QY 2080 rHisLeuGluGlyGluLeuArgProLysGlnProGlyProValLysLeuGlyGlyGluAl 2100
DB 6355 CCACCTGGAGGGGAGCTCGGCCCAAGCAGCAGCCCCCGTGAAGCTTGGCGGGGAGGC 6414
QY 2100 aAlaHisLeuProHisLeuArgProLeuProGluSerGlnProSerSerSerProLeuLe 2120
DB 6415 CGCCCACTCCCAACCTCGCGCGCTGCTGAGAGCCAGCCGCTGCTCAGCCCGCTGCT 6474
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QY 2140 rGluValIleThrGlnAspTyrThrArgHisHisProGlnGlnLeuSerAlaProLeuPr 2160
DB 6535 TGAGGTATCATCAGAGGACTACCCCGGCACCAACAGCAGCTCAGCGCACCCCTGCC 6594
QY 2160 oAlaProLeuTyrSerPheProGlyAlaSerCysProValLeuAspLeuArgArgProPr 2180
DB 6595 CGCCCCCTCTACTCTCCCTGGGSCCAGCTGCCCGCTCTGGACCTCCGCGGCCACCC 6654
QY 2180 oSerAspLeuTyrLeuProProProAspHisGlyAlaProAlaArgGlySerProHisSe 2200
DB 6655 CAGTGACCTCTACTCCCGCCCCCGACCATGGTGCCTCCCGCGCGGTGGCTCCCGCCACAG 6714
QY 2200 rGluGlyGlyLysArgSerProGluProAsnLysThrSerValLeuGlyGlyGlyGluAs 2220
DB 6715 CGAAGGGGCAAGAGTCTCAGAGCCAAACAGAGCTCGGTCTTGGGTGGTGGTGGGA 6774
QY 2220 pGlyIleGluProValSerProGluGlyMetThrGluProGlyHisSerArgSerAl 2240
DB 6775 CGGTATTGAACCTGTGTCCTCCACCGGAGGGCATGACGGAGCCAGGCGACTCCCGGAGTGC 6834
QY 2240 aValTyrProLeuLeuTyrArgAspGlyGluGlnThrGluProSerArgMetGlySerLy 2260
DB 6835 TGTGTACCCGCTGCTGTATCCGGGATGGGAAACAGACGGAGCCAGCAGATGGGCTCCAA 6894
QY 2260 sSerProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSerAsnSe 2280
DB 6895 GTCCTCAGGCAACACCGACCGCCCGCCGCTCTTTCAGCAAGCTGACCGAGAGCAACTC 6954
QY 2280 rAlaMetValLysSerLysGlnGluIleAsnLysLysLeuAsnThrHisAsnArgAs 2300
DB 6955 CGCCATGGTCAAGTCCAAAGCAAGAGATCAACAGAAAGCTGAACACCAACCAACCGGAA 7014
QY 2300 nGluProGluTyrAsnIleSerGlnProGlyThrGluIlePheAsnMetProAlaIleTh 2320
DB 7015 TGAGCTGTAATCAATATCAGCAGCTGGGAGCGGAGATCTTCAATATGCCCGCCATCAC 7074
QY 2320 rGlyThrGlyLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMe 2340
DB 7075 CGGACAGACGCTTATGACCTATAGAAGCCAGCGGCTGAGGAACATGCGCAGCAACCAAT 7134
QY 2340 tGlyLeuGluAlaIleArgLysAlaLeuMetGlyLysTyrAspGlnTrpGluLys 2360

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Db 7135 GGGGCTGAGGCCATAATTAGAAAGGCACCTCATCGGTAAATATATACCAAGTGGGAAGATC 7194
Qy rProProLeuSerAlaAlaSerAlaPheAsnProLeuAsnAlaSerAlaSerLeuProAlaA1 2380
Db 7195 CCGCGGCTCAGCGCCCAATGCTTTTAACTCTGATGCGAGTGGCGAGCTGCGCGTGC 7254
Qy 2380 aMetProileThrAlaAlaSerGlyArgSerAspHisThrLeuThrSerProGlyGlyG1 2400
Db 7255 TATGCCATAACCGCTGCTGACGAGCGAGTGACACACACTCACTCGCCAGGTGGCGG 7314
Qy 2400 yGlyAlaAlaValSerGlyArgProSerSerArgAlaAlaValSerProAlaProG1 2420
Db 7315 CCGGAAGGCCAAGGCTCTGCGACACCGAGCGAGCGGAAAGCCAAAGTCCCGGCGCGGG 7374
Qy 2420 yLeuAlaSerGlyAspArgProProSerValSerSerValHisSerGluGlyAspCysAs 2440
Db 7375 CTTGGCATCTGGGACCGCGCCACCTCTGCTCTCAGTGCATCTCGAGGAGACTGCAA 7434
Qy 2440 nArgArgThrProLeuThrAsnArgValTrpGluAspArgProSerSerAlaGlySerTh 2460
Db 7435 CCGCGGACCGGCTCACCAACCGCGGTGGAGGACAGAGCCCTCGTCCGAGGTTCCAC 7494
Qy 2460 rProPheProTyRhanProLeuMetArgLeuGlnAlaGlyValMetAlaSerProPr 2480
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Qy 2480 oProProGlyLeuProAlaGlySerGlyProLeuAlaGlyProHisAlaTrpAspG1 2500
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Qy 2500 uGluProLysProLeuLeuCysSerGlnTyRLeuThrLeuSerAspSerGlu 2517
Db 7615 GGAGCCCAAGCCACTGCTCTGCTGCGAGTACGAGACACTCTCCGACAGCGAG 7666
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RESULT 4

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US-09-819-104A-3
; Sequence 3, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND US$ THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 7521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7521)
US-09-819-104A-3
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Pred. No.: 0 Length: 7521
Score: 12978.00 Matches: 2487
Percent Similarity: 98.57% Conservative: 3
Best Local Similarity: 98.46% Mismatches: 9
Query Match: 98.21% Indels: 28
DB: 10 Gaps: 3
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US-09-522-753-5 (1-2517) x US-09-819-104A-3 (1-7521)

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Qy 1 MetSerGlySerThrGlnLeuValAlaGlnThrTrpAlaThrGluProAspGlyPro 20
Db 1 ATGTGGGGCTCCACAGCCCTGTGGCAGACAGGTGGAGGGGCCACTGAGCCCCCGCTACCCG 60
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Qy 21 ProHisSerLeuSerTyRProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
Db 61 CCCACAGCCCTTTCTACCCAGTGCAGATCCCGGACGACACACGAGCTCGGCTCCTG 120
Qy 41 GluTyRlnHisHisSerArgAspTyRAlaSerHisLeuSerProGlySerIleIleGln 60
Db 121 GAGTACAGCACCACTCCCGGAGTATGCTCTCCACCTGTCCCGGCTCCATCATTCAG 180
Qy 61 ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
Db 181 CCCACGGCGGAGGCCCTCCCTGCTGTCTGAGTTCACGCCCGGAATGAACGCTCCAG 240
Qy 81 GluLeuHisLeuArgProGluSerHisSerTyRLeuProGluLeuGlyLysSerGluMet 100
Db 241 GAGCTCCACCTGGCGGCGAGAGTCCCACTCATACCTGCCGAGCTGGGAAATCAGAGATG 300
Qy 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
Db 301 GAGTTCATTGAAGCAAGCGCCCTCGGCTAGAGTGTCTGCTGACCCCTGCTGCGACCG 360
Qy 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
Db 361 TCACCCCTGTGGCCACGGGCGAGCTGCGGGATCTGAAGACCTCACCAAGGACCGTAGC 420
Qy 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
Db 421 CTGACGGGCAAGCTGGAAACCGGTGTCTCCCGCCAGCCCGCCGACACTGACCCCTGAGCTG 480
Qy 161 GluLeuValProProArgLeuSerLysGluLeuIleGlnAsnMetAspArgValAsp 180
Db 481 GAGCTGTGTCGGCGCACGGCTGTCCAAGGAGGAGCTGATCCAGAACATGGACCGCGTGGAC 540
Qy 181 ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGlnLeu 200
Db 541 CGAGAGATCACTGTTAGAGCAGCAGATCTCTAAGCTGAAGAGAGACGACCAACGCTG 600
Qy 201 GluGluGluAlaLysProProGluProGluLysProValSerProProProIleGlu 220
Db 601 GAGGAGGAGGCTGCCAAGCGCGCGAGCTGAGAAAGCCCGTGTCCACCGCGCCCATCGAG 660
Qy 221 SerLysHisArgSerLeuValGlnIleIleTyRAspGluAsnArgLysLysAlaGluAla 240
Db 661 TCGAAGCAGCGCAGCTGTGTGCAGATCATCTACGACGAGAACCGGAAGAGGCTGAAGCT 720
Qy 241 AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyRAsnGlnPro 260
Db 721 GCACATCGGATTTCTGGNAGGCTTGGGGCCCCAGGTGGAGTGGCGCTGTACACACGCC 780
Qy 261 SerAspThrArgGlnTyRHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu 280
Db 781 TCCGACACCGCGCAGTATCATGAGAACATCAAAATAAACCCAGCGCATGCGGAAGAGCTA 840
Qy 281 IleLeuTyRPhelysArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCysGln 300
Db 841 ATCTTGTTACTTCAAGAGGAGGAATCAGCTCGGAACAATGGGAGAGAGATTTCTGCCAG 900
Qy 301 ArgTyRAspGlnLeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAspPro 320
Db 901 CGCTATGACCAAGCTCATGGAGGCTGGGAGAGAGAGTGGAGCGCATCGGAACACACCCC 960
Qy 321 ArgArgArgAlaLysGluSerLysValArgGluTyRTrpGluLysGlnPheProGluIle 340
Db 961 CGGCGGCGGCCCAAGGAGAGCAAGTTTCGCGAGTACTACGAGAAGCAGATTTCCCTGAGATC 1020
Qy 341 ArgLysGlnArgGlnLeuGlnArgMetGlnSerArgValGlyGlnArgGlySerGly 360
Db 1021 CGCAAGCAGCGGAGCTGCGAGGAGCGCATCGAG---AGGGTGGGCCCGCGGGCAGTGGG 1077
Qy 361 LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeuSer 380
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Qy 381 GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyR 400
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1138	GAGCAGGAGAACTGAGAGAGCAGATGCGCCAGCTGGCGCTGATCCGCCCATGCTGTAC	1197	Db
401	AspAlaAspGlnArgIleIysPheIleAsnMetAsnGlyLeuMetAlaAspProMet	420	Qy
1198	GAGCGTACAGCAGGAGGATCAAGTTCATCAATGAAAGCGGCTTATGGCCGACCCCATG	1257	Db
421	LysValTyrIysAspArgGlnValMetAsnMetTpsSerGluGlnGluIysGluThrPhe	440	Qy
1258	AAAGTGTACAAAGACCGCCAGGTTCATGACATGTGGAGTGAGCAGAGAGAGACCTTC	1317	Db
441	ArgGluIysPheMetGlnHisProIysAsnPheGlyLeuIleAlaSerPheLeuGluArg	460	Qy
1318	CGGAGAGTTCATGACGATCCCAAGAACTTTGGCTCATCGCATTCCTGGAGAGG	1377	Db
461	LysThrValAlaGluCysValLeuTyrTyrLeuThrIysAsnGluAsnTyrIys	480	Qy
1378	AAGACGTGGCTGAGTGGCTCTATTACTACTGACTAAGNAGATGAGAACTATAAG	1437	Db
481	SerLeuValArgArgSerTyrArgArgGlyIysSerGlnGlnGlnGlnGlnGln	500	Qy
1438	AGCTGTGTAGAGGAGCTATCGCGCGCGGCAAGAGCCAGCAGCAACAACAGCAGAG	1497	Db
501	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	520	Qy
1498	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1557	Db
521	AspGluIysGluIysGluIysGluIysGluIysGluIysGluIysGluIysGluIys	540	Qy
1558	GATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1617	Db
541	AspIysGluAspLeuLeuIysGluIysThrAspAspThrSerGlyLeuAspAsnAspGlu	560	Qy
1618	GACAAGGAGAGCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1677	Db
561	LysGluAlaValAlaSerLysGlyArgGlyThrAlaAsnSerGlnGlyArgGlyGly	580	Qy
1678	AAGGAGGCTGGGCTCCAAAGGCGCGAACTGCCAACAGCAGGAGGAGGAGGAGG	1737	Db
581	ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGluAlaIleThrProGlnGln	600	Qy
1738	CGCATCCCCGCTCAATGGTAAATGAGGCCAACAGCGAGGAGGAGGAGGAGGAG	1797	Db
601	SerAlaGluLeuAlaSerMetGluLeuAsnGluSerArgTpsThrGluGluGluMet	620	Qy
1798	AGCGCGAGCTGGCTCCATGAGCTGAATGAGAGTTCCTCTGACAGAGAGAGAAATG	1857	Db
621	GluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTpsSerAlaIleAlaArgMet	640	Qy
1858	GAACAGCCAGAAAGGTCTCTGGAAACACGCGCGCAACTGTCGCGCATCGCCGGATG	1917	Db
641	ValGlySerLysThrValSerGlnCysLysAsnPheTyrPheAsnTyrLysLysArgGln	660	Qy
1918	GTGGGCTCCAGACTGTGTGCGAGTGTAAAGAACTTCTACTTCAACTCAAGAGAGGAG	1977	Db
661	AnnLeuAspGluIleuGlnGlnHisLysLysLeuLysMetGluLysGluArgAsnAlaArg	680	Qy
1978	AACTCGATGAGATCTTGACGAGGAGCAAGCTGAAGATGGAGAGAGAGAGAGAGAG	2037	Db
681	ArgLysLysLysAlaProAlaAlaSerGluGluAlaAlaPheProValVal	700	Qy
2038	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2097	Db
701	GluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu	720	Qy
2098	GAGGATGAGGAGATGAGGCGTGGCGGTGAGGAAATGAGAGAGAGATGTTGGAGGAG	2157	Db
721	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740	Qy
2158	GCTGAA-----GCC	2166	Db
741	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaLys	760	Qy
12167	ACTGTCAACAAACAGCTCAGACACCGAGAGCATCCCTCTCTCACACTGAGCGCCGCAAG	2226	Db
761	AspThrGlyGlnAsnGlyProIysProAlaThrLeuGlyAlaAspGlyProProPro	780	Qy
2227	GACACAGGAGAGATGGGCCAAAGCCCGCCAGCCCTTGGCGCCGACCGGGCCACCCCA	2286	Db
781	GlyProProThrProPro-ArgArgThrSerArgAlaProIleGluProThrProAlaSe	800	Qy
2287	GGGCCACCCACCCACCCACCCAGGAGGACATCCCGGCC-CCCACCTGAGTCCACCCCGGCTC	2345	Db
800	rGluAlaThrGlyAlaProThrProProAlaProProSerProSerProSerProPr	820	Qy
2346	TGAAGCACCTTAGCCCTAGCCCTACGCCCCACCCAGCACCCCATTTCCCTTCCTCCTCC	2405	Db
820	oValValProIysGluIysGluGluThrAlaAlaAlaProProValGluGluGlu	840	Qy
2406	TGTGGTCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2465	Db
840	yGluGluGlnIysProProAlaAlaGluGluLeuAlaValAspThrGlyLysAlaGluGlu	860	Qy
2466	GGAGGAGCAGAAGCCCGCGCGCTGAGGAGCTGGCAGTGACACAGGAGGAGGAGGAGG	2525	Db
860	uProValIysSerGluCysThrGluGluAlaGluGluGlyProAlaLysGlyLysAspAl	880	Qy
2526	GCCCGTCAAGAGCGAGTGACCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2585	Db
880	aGluAlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysLysGluGlySe	900	Qy
2586	GGAGGCCCTGAGGCCACCGCGAGAGGGCGCTCAAGCAGAGAGAGAGAGAGAGAGAG	2645	Db
900	rGlyArgAlaThrThrAlaLysSerSerGlyAlaProGlnAspSerAspSerAlaTh	920	Qy
2646	CGGCAGGCGCCACCAAGAGAGAGCTCGGCGCGCCCGCCAGCAGCAGCAGCAGCAG	2705	Db
920	rCysSerAlaAspGluValAspGluAlaGluGlyGlyLysAsnArgLeuLeuSerPr	940	Qy
2706	CTGCAGTGACAGAGAGTGATGAGCGCGAGGCGCGCGCAGCAAGAACCGGCTGCTGCC	2765	Db
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2766	AAGGCCAGCTCTCTCACCCGACTGGGAGACCCCGCGGCAATGCTCACCCCAAGAGCC	2825	Db
960	oLeuAspLeuLysGlnLeuLysGlnArgAlaAlaIleProProIleGlnValThrLy	980	Qy
2826	ACTGGACCTGAAGCAGCTGAAGCAGCAGCGCTGCCATCCCCCATCCAGTCAACAA	2885	Db
980	sValHisGluProProArgGluAspAlaAlaProThrLysProAlaProAlaProPr	1000	Qy
2886	AGTCCATGAGCCCCCGCGAGGAGCAGCTCCACCAAGCAGCTCCCGCCAGCCCAAC	2945	Db
1000	oProProGlnAsnLeuGlnProGluSerAspAlaProGlnGlnProGlySerSerProAr	1020	Qy
2946	GCCACGCGCAAAACCTGACGCGGAGAGCGCCCTCAGCAGCTTGGCAGCGGAGCGCCG	3005	Db
1020	gGlyLysSerArgSerProAlaProProAlaAspLysGlu-----	1033	Qy
3006	GGGACAGAGCAGAGAGCGCGCCACCCCGCGCGCAGAGGAGGAGAGAGAGAGAGAG	3065	Db
1034	----AlaPheAlaAlaGluAlaGlnLysLeuProGlyAspProProCysTpsThrSerG	1052	Qy
3066	CCCAGGCTTCGACGCGAGGCGCCAGAGCTGCTGGGAGACCCCTTGTGGACTTCCGG	3125	Db
1052	yLeuProPheProValProProArgGluValIleLysAlaSerProHisAlaProAspPr	1072	Qy
3126	CCTGCCCTTCCCGTGGCGCCCGCTGAGGTGATCAAGGCTCCCGCATGCGCGAGCCC	3185	Db
1072	oSerAlaPheSerTyrAlaProProGlyHisProLeuProLeuGlyLeuHisAspThrAl	1092	Qy
3186	CTCAGGCTTCTCTACGCTCCACTGGTCAACCCACTGCCCTGGGCTCCATGACACTGC	3245	Db
1092	aArgProValLeuProArgProProThrIleSerAsnProProProLeuIleSerAl	1112	Qy
3246	CCGCGCGCTCTGCGCGCGCCACCCACCATCTCCAAACCCCGCTTCCCTCATCTCTGC	3305	Db

Qy	1112	aLysHisProSerValLeuGluArgGlnIleGlyAlaIleSerGlnGlyMetSerValG1	1132
Db	3306	CAAGCACCCAGCGTCTCCAGAGGCAATAGGTGCCATCTCCCAAGGAATGTCCGTCCA	3365
Qy	1132	nLeuHisValProTyrSerGluHisAlaLysAlaProValGlyProValThrMetGlyLe	1152
Db	3366	GCTCCAGTCCCGTACTCAGAGCATGCCAAGGCCCGCGTGGCCCTGTCCACATGGGGCT	3425
Qy	1152	uProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGluInLe	1172
Db	3426	GCCCTGCCCATGACCCCAAAAGCTGGCACCTTTCAGCGGAGTGAAGCAGGACAGCT	3485
Qy	1172	uSerProArgGlyGlnAlaGlyProProGluSerLeuGlyValProThrAlaGlnGluAl	1192
Db	3486	GTCCCCACGGGGCCAGGCTGGGCCACCGGAGAGCTGGGGTGGCCACAGCCACGAGGAGGC	3545
Qy	1192	aSerValLeuArgGlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyI1	1212
Db	3546	GTCCGTGCTGAGAGGAGCAGCTCTGGGCTCAGTTCCGGGGGGAAGCATCAACAAAGGCAT	3605
Qy	1212	eProSerThrArgValProSerAspSerAlaIleThrTyrArgGlySerIleThrHisG1	1232
Db	3606	TCCAGCACAGGCTGCCCTCGGACAGGCCATCACATACCGCGGCTCCATCACCACGG	3665
Qy	1232	YThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIleGlyGluAspSerPr	1252
Db	3666	CACGCCAGCTGACGTCGTCTACAAAGGCACCATCACAGGATCATCCGCGGAGCAGACCC	3725
Qy	1252	oSerArgLeuAspArgGlyArgGluAspSerLeuProLysGlyHisValIleTyrGluG1	1272
Db	3726	GAGTCGCTTGACCGCGCGGGAGGACAGCGCTGCCAAAGGGCCACGTCATCTACGAAGG	3785
Qy	1272	YLysLysGlyHisValLeuSerTyrGluGlyGlyMetSerValThrGlnCysSerLysG1	1292
Db	3786	CAAGAAGGGCCACGCTTGTCTTGAAGGTGGCATGTCTGTGACCCAGTGTCTCAAGGA	3845
Qy	1292	uAspGlyArgSerSerGlyProProHisGluThrAlaAlaProLysArgThrTyrAs	1312
Db	3846	GGACGGCAGAAGCAGCTCAGSACCCCCCATGAGACGGCGCCGCCCAAGCGCCTATGA	3905
Qy	1312	pMetMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGlyLeuMetG1	1332
Db	3906	CATGATGAGGGCGCGTGGCGAGAGCCATCTCTCAGCCAGCATCGAAGGTCTCATGGG	3965
Qy	1332	YArgAlaIleProProGluArgHisSerProHisHisLeuLysGluGlnHisIleAr	1352
Db	3966	CCGTGCCATCCCGCGGAGCGACACAGCCCCCACCACCTCAAGAGCAGCACCATCCG	4025
Qy	1352	gGlySerIleThrGlnGlyIleProArgSerTyrValGluAlaGlnGluAspTyrLeuAr	1372
Db	4026	CGGTCCATCACAAAGGGATCCCTCGTCTCTAGCTGGAGGCA CAGGAGGACTACCTGCG	4085
Qy	1372	gArgGluAlaLysLeuLysArgGluGlyThrProProProProProSerArgAs	1392
Db	4086	TCGGGAGGCCAAGCTCTAAAGCGGGAGGCGAGCCCTCCGCCCCCAGCCCTCACGGGA	4145
Qy	1392	pLeuThrGluAlaTyrLysThrGlnAlaLeuGlyProLeuLysLeuLysProAlaHisG1	1412
Db	4146	CCTGACCGAGGCTTACAAGACGAGGCCCTTGGGCCCTTGAAGCTGAAGCGGGCCCATGA	4205
Qy	1412	uGlyLeuValAlaThrValLysGluAlaGlyArgSerIleHisGluIleProArgGluG1	1432
Db	4206	GGGCTGTGGCCACGCTGAAGGAGGCGGGCGGCTCCATCATGAGATCCCGCGGAGGA	4265
Qy	1432	uLeuArgHisThrProGluLeuProLeuAlaProArgProLeuLysGluGlySerIleTh	1452
Db	4266	GCTGCGGCACACGCCCCGAGTGTGCCCTTGGCCCCCGCGCGCTCAAGGAGGGCTCCATCAC	4325
Qy	1452	xGlnGlyThrProLeuLysTyrAspThrGlyAlaSerThrThrGlySerLysLysHisAs	1472
Db	4326	GCAGGGCACCCCGCTCAAGTACGACACCGCGCGGTCCACCACCTGGCTCCAAAAGCACGA	4385

Qy	1472	pValArgSerLeuIleGlySerProGlyArgThrPheProProValHisProLeuAspVa	1492
Db	4386	CGTACGCTCCCTCATCGCAGCCCGCGCGAGACTTCCACCCGTGACCCGCTGGATGT	4445
Qy	1492	lMetAlaAspAlaArgAlaLeuGluArgAlaCysTyrGluLysSerLeuLysSerArgPr	1512
Db	4446	GATGGCCGAGCCCGGCACTGGAACTGTCTGTCTACGAGAGAGCTTGAAGAGCCGGCC	4505
Qy	1512	oGlyThrAlaSerSerGlyGlySerIleAlaAArgGlyAlaProValIleValProG1	1532
Db	4506	AGGACCCGCGCAGCAGCTCGGGGGTCCATTTGCGCGCGCGCCCGCTTGTGCTGAT	4565
Qy	1532	uLeuGlyLysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaG1	1552
Db	4566	GCTGGGTAAAGCCGCGCAGAGCCCTGACCTATGAGGAGCACCGGGCACCCCTTTCGCG	4625
Qy	1552	YHisLeuProArgGlySerProValThrMetArgGluProThrProArgGluG1	1572
Db	4626	CCACCTCCACAGAGTTCCGCCGTGACCATGCGGGAGCCACCGCGGCTTGCAGGAGGG	4685
Qy	1572	YSerLeuSerSerSerLysAlaSerGlnAspArgLysLeuThrSerThrProArgGluI1	1592
Db	4686	CAGCTTTCTCCAGCAAGGCATCCAGAGACCGAAAGCTGACGTGACGCTCGTGAGAT	4745
Qy	1592	eAlaLysSerProHisSerThrValProGluHisHisProHisProLysSerProTyrG1	1612
Db	4746	CGCCAAAGTCCCGCACAGCACCGTCCCGGAGCACACCCACACCCCTCTCGCCCTATGA	4805
Qy	1612	uHisLeuLeuArgGlyValSerGlyValAspLeuTyrArgSerHisIleProLeuAlaPh	1632
Db	4806	GCACCTGCTTCCGGGGGTGAGTGGCGTGGACCTGTATCGAGGCCACATCCCTTGGGCTT	4865
Qy	1632	eAspProThrSerIleProArgGlyIleProLeuAspAlaAlaAlaIaTyrTyrLeuPr	1652
Db	4866	CGACCCACCTCCATACCCCGCGGCATCCCTCTGGAGCGAGCGCTGCTACTACTGCTCC	4925
Qy	1652	oArgHisLeuAlaProAsnProThrTyrProHisLeuTyrProProTyrLeuIleArgG1	1672
Db	4926	CCGACACCTGGCGCCCAACCCACCTACCGCGACCTGTACCCACCTTACCTCATCCGCGG	4985
Qy	1672	YThrProAspThrAlaAlaLeuGluAsnArgGlnThrIleIleAsnAspTyrIleThrSe	1692
Db	4986	CTACCCCGGACACGGCGCGCTGGAGAACCGGCGACCATCATCAATGACTACATCACCCTC	5045
Qy	1692	rGlnGlnMetHisHisAsnThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArgG1	1712
Db	5046	GCAGCAGATGCACACACACGCGCCACCGCATGGCCCGGAGCTGATATGCTGAGGGG	5105
Qy	1712	YLeuSerProArgGluSerSerLeuAlaLeuAsnTyrAlaAlaGlyProArgGlyIleI1	1732
Db	5106	CCTCTCGCCCCGAGTCTCTCGTGGCACTCAACTACGCTGCGGGTCCCGGAGGCATCAT	5165
Qy	1732	eAspLeuSerGlnValProHisLeuProValLeuValProThrProThrProGlyThrProAl	1752
Db	5166	CGACCTGTCTCCAGTGCACACCTCGCTGTCTGTGCCCCCGGACACAGGACCCCGAGC	5225
Qy	1752	aThrAlaMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSerArgHi	1772
Db	5226	CACCGCCATGACCGCGCTTGCTTACCTCCCAACCGCGCCCCCGGCTTACAGCGCGCCA	5285
Qy	1772	sSerSerSerProLeuSerProGlyProThrHisLeuThrLysProThrThrThrSe	1792
Db	5286	CAGCAGCTCCCACTCTCCCGCAGAGGTCCAAACACACTTGCACAAAACCAACACCATGC	5345
Qy	1792	rSerSerGluArgGluArgAspArgAspArgGluArgAspArgAspArgGluArgGluLy	1812
Db	5346	CTCGTCCGAGCGGAGCGAGACCGGGATCGAGAGCGGAGCCGGATCGGAGCGGAGAAA	5405
Qy	1812	sSerIleLeuThrSerThrThrThrValGluHisAlaProIleIleIleIleIleIleIleI	1832
Db	5406	GTCTATCTCTCATCTCCACACGAGCGTGGAGACGACCCCATCTGGAGACATCTGGTACAGA	5465
Qy	1832	uGlnSerSerGlySerSerGlySerGlyGlyGlyGlyGlySerSerSerArgProAl	1852


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; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8686
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(7677)
US-09-819-104A-1

Alignment Scores:
Pred. No.: 0 Length: 8686
Score: 12978.00 Matches: 2487
Percent Similarity: 98.57% Conservative: 3
Best Local Similarity: 98.46% Mismatches: 9
Query Match: 98.21% Indels: 28
DB: 10 Gaps: 3

US-09-522-753-5 (1-2517) x US-09-819-104A-1 (1-8686)

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QY 21 ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
DB 217 CCCACAGCCTTTCCTACCCAGTGCAGATGCCCGGACGACAGCGTCCGGCTCCTG 276
QY 41 GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleIleGln 60
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QY 61 ProGluArgArgProSerLeuLeuSerGluPheGlnProGlyAenGluArgSerGln 80
DB 337 CCCAGCGGGAGGCGCTCCCTGCTGTCTGAGTTCAGGCGCGGGAATGAACGGTCCCAG 396
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
DB 397 GAGCTCCACTGCGGCAGAGTCCCACTATACCTGCCAGCTGGGGAATCAGAGATG 456
QY 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
DB 457 GAGTTCATTGAAGCAAGCGCCCTCGGCTAGAGCTGCTGACCCCTGCTGCGACCG 516
QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
DB 517 TCACCCCTGCTGGCCAGCGGCCAGCTGCGGGAATCTGAAGACCTCACCAAGGACCGTAGC 576
QY 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
DB 577 CTGACGGGCAAGCTGGAACCGGTGTCTCCCGGAGCCCCCGCACACTGACCTCGAGCTG 636
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAenMetAspArgValAsp 180
DB 637 GAGCTGTGCGCGCAGCGCTGTCCAGGAGGAGCTATCCAGAACATGAGACCGCGTGGAC 696
QY 181 ArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnLeu 200
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DB 1894 CGCATCACCCTGCTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCCAGCAG 1953

817 TCGAAGCACCGCAGCCTGCTGTCAGATCATCTACGACGAGAACCGGAAGAGCGTGAAGCT 876
241 AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro 260
877 GCACATCGGATCTCGAAGCGCTGGGGCCCCAGGTGGAGCTGCGCTGTACACACCGAGCCC 936
261 SerAspThrArgGlnTyrHisGluAenIleLysIleAenGlnAlaMetArgLysLysLeu 280
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1774 GACNAGAGAGACTCTCTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1833
561 LysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgArgLysGly 580
1834 AAGGAGGCTGTGCGCTCCAAAGCGCCCAAACTGCCAACAGCAGCAGGAGAGAGAGAG 1893
581 ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluGluAlaIleThrProGlnGln 600
1894 CGCATCACCCTGCTCAATGGCTAATGAGGCCAACAGCGAGGAGGCCATCACCCCCCAGCAG 1953
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DB 1954 AGCGCCGAGCTGGCCCTCCATGAGCTGAATGAGAGTTCTCGCTGGACAGAGAGAAATG 2013
QY 621 GluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTTPSerAlaAlaArgMet 640
DB 2014 GAACAGCCAGCAAGAAAGTCTCTCGGAACACGCGCCCACTGGTTCGCCCATCGCGGATG 2073
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QY 681 ArgLysLysLysLysAlaProAlaAlaAlaSerGluAlaAlaPheProValVal 700
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DB 2254 GAGGATGAGGAGTGGAGGCGCTCGGCGTGAACGGGAATGAGAGAGATGTTGGAGGAG 2313
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Db	4122	CCGTGCCATCCCGCGGAGCGACACAGCCGCCACCACTCAAGAGCAGCACCAATCCG	4181	
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Qy	1472	pValArgSerLeuIleGlySerProGlyArgThrPheProProValHisProLeuAspVa	1492	
Db	4542	CGTAGCTCCCTCATCGGCACCCCGCGCGGACGTTCCACCCCGTGACCCGCTGGATGT	4601	
Qy	1492	lMetAlaAspAlaArgAlaLeuGluAArgAlaCyTyrGluSerLeuLysSerArgPr	1512	
Db	4602	GATGGCCGACCCCGGCACCTGGAAACGTGCCTGTCTAGCAGGAGAGCCTGAAGAGCGCGCC	4661	
Qy	1512	oGlyThrAlaSerSerSerGlyGlySerIleAlaArgGlyAlaProValIleValProG1	1532	
Db	4662	AGGGACCGCCAGCAGCTCGGGGGCTCCATTGGCGCGGGCGCCCGGTCAATTGTCCTGA	4721	
Qy	1532	uLeuGlyLysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaG1	1552	
Db	4722	GCTGGGTAAAGCCGCGGCAGACGCCCTCGACCTATGAGGACACACGGGGCACCCCTTGGCCG	4781	
Qy	1552	yHisLeuProArgGlySerProValThrMetArgGluProThrProArgLeuGlnGluG1	1572	
Db	4782	CCACCTCCACAGAGTTCCGCCGTGACCATCGGGAGCCCAACGCGCGCCCTGCAGGAGGG	4841	
Qy	1572	ySerLeuSerSerSerLysAlaSerGlnAspArgLysLeuThrSerThrProArgGluI1	1592	
Db	4842	CAGCCTTTCTGTCAGACAGGACATCCACGAGACCGAAAGCTCAGCTGACGCTCGTGAGAT	4901	
Qy	1592	eAlaLysSerProHisSerThrValProGluHisHisProHisProLysSerProTyrG1	1612	
Db	4902	CGCCAAAGTCCCGCACAGCACCGTGGCCGAGCACCAACCCATCTCGCCCTATGA	4961	
Qy	1612	uHisLeuLeuArgGlyValSerGlyValAspLeuTyrArgSerHisIleProLeuAlaph	1632	
Db	4962	GCACCTGCTCGGGCGGTGAGTGGGTGGACCTGTATCGAGGCCACATCCCTCGGCCTT	5021	
Qy	1632	eAspProThrSerIleProArgGlyIleProLeuAspAlaAlaAlaTyrTyrLeuPr	1652	
Db	5022	CGACCCCACTCCATACCCCGCGGATCCCTCTCGACGCGAGCGCTGCCCTACCTACCTGGC	5081	
Qy	1652	oArgHisLeuAlaProAsnProThrTyrProHisLeuTyrProProTyrLeuIleArgG1	1672	
Db	5082	CCGACACTGGCCCCCAACCCCACTACCGCACCTGTACCCACCTTACCTATCCGCGG	5141	
Qy	1672	yTyrProAspThrAlaAlaLeuGluAAsnArgGlnThrIleIleAsnAspTyrIleThrSe	1692	

D	b	5142	CTACCCCGACACGGCGGCGTGGAGAAACC CGCAGACCATCATCAATGACTACATCACCTC	5201
Q	y	1692	rGlnClnMetHisHisAenThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArgGl	1712
D	b	5202	GCAGCATGCACACACACGCCCGCCATGGCC CAGGAGTCGTATGCTGAGGG	5261
Q	y	1712	yLeuSerProArgGluSerSerLeuAlaLeuAenTy rAlaAlaGlyProArgGlyLeIlel	1732
D	b	5262	CCTCTCGCCCGGAGTCTCGTGCGTGGCACTCA CTACGCTCGGGTCCCCGAGCATCAT	5321
Q	y	1732	eAspLeuSerClnValProHisLeuProValLeuVal ProProThrProGlyThrProAl	1752
D	b	5322	CGACCTGTCCCAAGTGCACACCTGCTGCTGCT GCTGCTGCCCGCACACAGCACCCCAGC	5381
Q	y	1752	aThrAlaMetAspArgLeuAlaTy rLeuProThrAlaProGlnProPheSerSerArgHi	1772
D	b	5382	CACGCCATGAGCGCCTTGCCCTACCTCCCA CCGCGCCCCAGCCCTTCAGCAGCCGCCA	5441
Q	y	1772	sSerSerSerProLeuSerProGlyGlyProThrHis LeuThrLysProThrThrThrSe	1792
D	b	5442	CAGCAGCTCCCACTCTCCCGAGGAGTCCAACA CACTTGACAAAAACCAACCAACCCAGTC	5501
Q	y	1792	rSerSerClnuArgGluArgAspArgAspGluuAr gAspAspArgGluArgGluLy	1812
D	b	5502	CTCGTCGAGCGGAGGAGACCGGGATCGAGAG CCGGATCGGAGCGGGGA	5561
Q	y	1812	sSerIleLeuThrSerThrThrValGluHisAlaPr oIleTrpArgProGlyThrGl	1832
D	b	5562	GTCATCTCTACGTCCACCAAGCGTGGAGCAGCA CCCATCTGGHAGACTGGTACAGA	5621
Q	y	1832	uGlnSerSerGlySerSerGlyGlyGlyGlyGly GlyGlySerSerArgProAl	1852
D	b	5622	GCAGCAGCGGCAGCAGCGCAGCAGCGCGGG GTGGGGCAGCAGCAGCGCCCCCGC	5681
Q	y	1852	aSerHisSerHisAlahisGlnHisSerProLlis eSerProArgThrClnAspAlaLeuGl	1872
D	b	5682	CTCCACTCCCATGCCCCACACAGACTCGCCCA TCTCCCCCTCGAACCCAGATGCCCTCCA	5741
Q	y	1872	nGlnArgProSerValLeuHisAenThrGlyMetL ysGlyIleIleThrAlaValGluPr	1892
D	b	5742	GCAGAGACCCAGTGTGTTTACACACACAGCAT GAAGGTATCATCACCGCTGTGGAGCC	5801
Q	y	1892	oSerLysProThrValLeuArgSerThrSerThrS erSerProValArgProAlaAlaTh	1912
D	b	5802	CAGCAAGCCCAACGGTCTCTGAGTCCACTCCAC CTCCTCCACCGCTTCGCCAGCTGCCAC	5861
Q	y	1912	xPheProProAlaThrHisCy sProLeuGlyGlyTh rLeuAspGlyValTy rProThrLe	1932
D	b	5862	ATTCCCACTGCCACCACTGCCACTTGGCGGC ACCTCGATGGGGTCTTACCCCTACCTC	5921
Q	y	1932	uMetGluProValLeuLeuProLysGluAlaPro AArgValAlaArgProGluArgProAr	1952
D	b	5922	CATGGAGCCCGTCTTGTCTGCCAAGAGGCCCC CC GGSTCGCCCGGCACAGCGGCCCGC	5981
Q	y	1952	gAlaAspThrGlyHisAlaPheLeuAlaLysPro P roAlaArgSerGlyLeuGluProAl	1972
D	b	5982	AGCAGACACCGGCCATSCCTTCTCGCCAAGCC CCCCAGCCCGCTCGCGGCTGGAGCCCGC	6041
Q	y	1972	aSerSerProSerLysGlySerGluProArgProLe uValProProValSerGlyHisAl	1992
D	b	6042	CTCTCCCGCCAGCAAGGGCTCGAGGCCCGCCG CCCCCTAGTGCCTCTGTCTCTGGCCACGC	6101
Q	y	1992	aThrIleAlaArgThrProAlaLysAenLeuAlaP roHisEHisAserProAspProPr	2012
D	b	6102	CACCATCGCCCGCACCCCTCGGAAGAACCTCG CACCTTCACACGCCAGCCCGGACCCGCC	6161
Q	y	2012	oAlaProProAlaSerAlaSerAspProHisAr gGluLyThrClnSerLysProPheSe	2032
D	b	6162	GGCGCCACCTGCCTCGSCCTCGAACCCGCAC CCGGAAAAGACTCAAAGTAACCCCTTTTC	6221
Q	y	2032	rIleGlnGluLeuGluLeuArgSerLeuGlyTy rHisGlySerSerTy rSerProGluGl	2052
D	b	6222	CATCCAGAACTGAACTCCGTTCTCTGGGTATC CACGCGCAGCAGCTTACAGCCCCGHAAG	6281

Qy	81	GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet	100
Db	397	GAGCTCCACCTCGCGCCAGAGTCCCACTCATACCTGCGGAGCTGGGGAACTCAGAGATG	456
Qy	101	GlupheIleGluSerLysArgProArgLeuCluLeuLeuProAspProLeuLeuArgPro	120
Db	457	GAGTTTCATTGAAGCAAGCGCCCTCGCGTAGAGCTGTGCTGACCCCTGCTCGACCG	516
Qy	121	SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer	140
Db	517	TCACCCCTGTGGCCACGGGCCAGCTCGGGGATCTGAAGACCTCCACAGGACCGTAGC	576
Qy	141	LeuThrGlyLysLeuGluProValSerProProSerProProHisIleThrAspProGluLeu	160
Db	577	CTGACGGGCAAGCTGGAAACCGGTGTCTCCGCCACGCCCCCGCACACTGACCCCTGAGCTG	636
Qy	161	GluLeuValProProArgLeuSerLysGluCluLeuIleGlnAsnMetAspArgValasp	180
Db	637	GAGCTGGTGGCCGCCACCGCTGTCCAAGAGAGAGTGTATCCAGAACATGGACCCGCGTGGAC	696
Qy	181	ArgGluIleThrMetValGluGlnGlnIleSerLysLysLeuLysLysGlnGlnLeu	200
Db	697	CGAGAGATCACCATGGTAGACAGCAGATCTCTTAAGCTGAAGAGAGAGCAGCAACAGCTG	756
Qy	201	GluGluAlaAlaLysProProGluProGluLysProValSerProProIleGlu	220
Db	757	GAGGAGGAGGCTGCAAGCGCCGCCAGCTCAGAAGCCCGTGTCAACGCCGCCATCGAG	816
Qy	221	SerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGluAla	240
Db	817	TCGAAGCACCGCAGCCTGGTGCAAGTCACTTACACAGAGAACCGGAAGAAGCTGAAGCT	876
Qy	241	AlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGlnPro	260
Db	877	GCACATCGGATCTTGGAAGGCTCGGGGCCCCAGCTGGAGCTGCGCTGTATACACCGCCC	936
Qy	261	SerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnAlaMetArgLysLysLeu	280
Db	937	TCCGACACCCGGCAGTAGTATCATGAGAACATCAAAATAAACACGAGCGATCGGAGAGAGCTA	996
Qy	281	IleLeuTyrPheLysArgArgAsnHisAlaArgLysGlnTyrLysGlnLysPheCysGln	300
Db	997	ATCTTGACTTCAAGAGGAGAAATCAGCTCGGAACAATGGGAGCAGAAAGTTCTGCGCAG	1056
Qy	301	ArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAsnPro	320
Db	1057	CGCTATCACCACTCATGGAGGCTCGGAGAGAGAGGTGGAGCGCATCGAGACACACCCC	1116
Qy	321	ArgArgAlaLysGluSerLysValArgGlnTyrTyrGluLysGlnPheProGluIle	340
Db	1117	CGCGCGCGGCGCAAGGAGAGCAAGGTTTCGCGAGTACTACGAGAAGCAGTTTCCCTGAGATC	1176
Qy	341	ArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgValGlyGlnArgGlySerGly	360
Db	1177	CGCAAGCAGCGCAGCTGCGAGGCGCATGCGAG--AGGGTGGCGCCAGCGGGCGCAGTGGG	1233
Qy	361	LeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeuSer	380
Db	1234	CTGTCCATGTCCCGCGCCGAGCGAGCAAGAGGTGTACAGATCATCATGATGGCTCTCA	1293
Qy	381	GluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeuTyr	400
Db	1294	GAGCAGGAGAACTGGAGAGCAGATGCGCCAGCTGGCCGTGTATCCCGCCCATGCTGTATC	1353
Qy	401	AspAlaAspGlnGlnArgIleLysPheIleAsnMetAsnGlyLeuMetAlaAspProMet	420
Db	1354	GAGCTTCACAGCAGCGCATCAAGTTTCATCAACATGAACCGGCTTATGGCGCGACCCCATG	1413
Qy	421	LysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluLysGluThrPhe	440
Db	1414	AAGGTGTCAAGAGCCGCCAGGTCTATGAACATGTGGAGTGTGACGAGAGAGGACCTTC	1473
Qy	441	ArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIleAlaSerPheLeuGluArg	460

1474	CGGAGAGAAGTTTCATGCAGCAGTCCCAAGAACTTTTGGCGTGTGCGCATCATTTCTCTGGAGAGG	1533
461	LyethrValAlaGluCysValLeuTyrTyrTyrLeuThrLysLysAsnGluAsnTyrLys	480
1534	AAGACAGTGGCTGAGTGGTGGCTTCTATTACTCTGACTAAGAAGAAATAGAACTATAAG	1593
481	SerLeuValArgArgSerTyrArgArgGlyLysSerGlnGlnGlnGlnGlnGlnGln	500
1594	AGCCTGGTGAGCGGAGCTATCGCGCGCGCAAGAGCCAGCAGCAACAACAGCAGCAG	1653
501	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	520
1654	CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	1713
521	AspGluLysGluLysGluLysGluAlaGluLysGluLysGluLysGluLysGluLys	540
1714	GATGAGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1773
541	AspLysGluAspLeuLeuLysGluLysThrAspAspThrSerGlyGluAspAsnAspGlu	560
1774	GACAAAGAGACCTCCTCAAGAGAGAGACAGACACACCTCAGGGGAGGACACAGCAG	1833
561	LysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgArgLysGly	580
1834	AAGGAGGCTGTGGCTCTCAAAAGGCGCAAACTGCCAACAGCCAGCGGAGAGCAAGGC	1893
581	ArgIleThrArgSerMetAlaAsnGluAlaAsnSerGluLysLysLysLysLysLys	600
1894	CGATCACCCGCTCAATGGCTAATGAGGCCAAAGAGGAGGAGGAGGAGGAGGAGG	1953
601	SerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTrpThrGluGluMet	620
1954	AGCGCCGAGTGGCTCCATGGAGCTGAATGAGATTCTCGCTGGACAGAGAAGAAATG	2013
621	GluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTrpSerLysLysLysLys	640
2014	GAACAACAGCAAGAAAGGTTCTCTGGAAACAGCGCGCAACTGGTGGCCATCGCCGATG	2073
641	ValGlySerLysThrValSerGlnCysLeuAsnPheTyrPheAsnTyrLysLysArgGln	660
2074	GTGGGCTCCAAAGACTGTGTGCGAGTGAAGACTTCTTACTTCAACTACAGAAGAGGCG	2133
661	AsnLeuAspGluIleLeuGlnGlnHisLysLeuLysMetGluLysGluArgAsnAlaArg	680
2134	AACCTCGATGAGATCTTGACAGCAGCAAGCTGAAGATGGAGAAGGAGAGCAAGCGCG	2193
681	ArgLysLysLysLysAlaProAlaAlaSerGluGluAlaAlaPheProValVal	700
2194	AGGAAGAAGAAGAAAGCGCGCGCGCGCGCAGCGAGAGGCTGCATTCCCGCGCTGGTG	2253
701	GluAspGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGluGlu	720
2254	GAGATGAGGAGATGAGGCGGTGGCGGTGAGCGGAATGAGGAGGAGATGGTGGAGAGG	2313
721	AlaGluAlaLeuHisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAla	740
2314	GCTGAA-----GCC	2322
741	ThrValAsnAsnSerSerAspThrGluSerIleProSerProHisThrGluAlaLys	760
2323	ACTGTCAACAACAGCTCAGACCGGAGAGCATCCCTCTCTCCTCAGCTGAGGCGCGCAAG	2382
761	AspThrGlyLysGlnAsnGlyProLysProAlaThrLeuGlyAlaAspGlyProProPro	780
2383	GACACAGGCGAGAAATGGCGCCCAAGCCCCCAGCCACCTGGCGGCCGAGCGGCCACCC	2442
781	GlyProProThrProProArgArgThrSerArgAlaProIleGluProThrProAlaSer	800
2443	GGGCCACCCACCCACCCACCGGAGGACATCCCGGCC-CCCACTGAGTCCACCCCGGCTC	2501
800	rGluAlaThrGlyAlaProThrProProAlaProProSerProSerAlaProProPro	820

QY 1532 uLeuGlyLysProArgGlnSerProLeuThrThrGluAspHisGlyAlaProPheAlaG 1552
DB 4722 GCTGGGTAAAGCCGCGCAGAGCCCTTACATATAGGACACACGGGGACCCCTTTCGGG 4781
QY 1552 yHisLeuProArgGlySerProValThrMetArgGluProThrProArgLeuGlnGlu 1572
DB 4782 CCACCTCCCAACAGAGTTCGGCGGTGACCATGCGGGAGCCACCGCGCGCTGAGAGGG 4841
QY 1572 ySerLeuSerSerSerLysAlaSerGlnAspArgLysLeuThrSerThrProArgGluI 1592
DB 4842 CAGCCTTCCTCAGCAGAGCATCCAGAGCCGAAAGCTGACGTGACGGCTCGTGAGAT 4901
QY 1592 eAlaLysSerProHisSerThrValProGluHisHisProHisProLleSerProTyrG 1612
DB 4902 CGCCAAAGTCCCGCAGACACCGTGGCGGAGCCACCCACACCCCATCTCGCCCTATGA 4961
QY 1612 uHisLeuLeuArgGlyValSerGlyValAspLeuTyrArgSerHisGlyProLeuAla 1632
DB 4962 GCACCTGCTTCGGGGGTGAGTGGCGGTGACCTGTATCGCAGGCACATCCCTCGGCC 5021
QY 1632 eAspProThrSerIleProArgGlyIleProLeuAspAlaAlaAlaValTyrTyrLeuPr 1652
DB 5022 CGACCCACCTTCATACCCCGCGGCATCCCTCTGGACGAGCGCTGCTACTACCTGCC 5081
QY 1652 oArgHisLeuAlaProAsnProThrTyrProHisLeuTyrProTyrLeuIleArgG 1672
DB 5082 CCGACACCTGGCCCCCAACCCACCTACCGCGACCTGTATCCACCCCTACCTCATCCGCG 5141
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QY 1692 rGlnGlnMetHisHisAsnThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArg 1712
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QY 1712 yLeuSerProArgGluSerSerLeuAlaLeuAsnTyrAlaAlaGlyProArgGlyIleI 1732
DB 5262 CCTCTCGCCCGCGAGTCTCGTGGCCTCACTACGCTGCGGGTCCCGCGAGCATCAT 5321
QY 1732 eAspLeuSerGlnValProHisLeuProValLeuValProProThrProGlyThrProAl 1752
DB 5322 CGACCTGTCCCAAGTGCCACACCTGCTGTGCTCGTGGCCCGCCACACCGACGCCCG 5381
QY 1752 aThrAlaMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSerArgH 1772
DB 5382 CACCGCATGGACCGCTTCCCTACCTCCACCGCGCCCGCCGCTTACGACGCGCCCA 5441
QY 1772 sSerSerProLeuSerProGlyGlyProThrHisLeuThrLysProThrThrThrSe 1792
DB 5442 CAGCAGCTCCCACTCTCCCGAGAGGTCCACACACCTTGACAAACCAACACACCGTC 5501
QY 1792 rSerSerGluArgGluArgAspArgArgGluArgAspArgAspArgGluArgGlu 1812
DB 5502 CTCGTCCGAGCGGAGCGAGACCGGGATCGAGAGCGGGATCGGGAGCGGGAGAA 5561
QY 1812 sSerIleLeuThrSerThrThrValGluHisAlaProIleTrpArgProGlyThrG 1832
DB 5562 GTCCATCTCAGCTCACACACGAGCGGTGGAGACGACCCATCTGGAGACCTGGTACGA 5621
QY 1832 uGlnSerSerGlySerSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG 1852
DB 5622 GCAGACGAGCGGACGAGCGGACGAGCGCGGGGTGGGGGAGCAGCAGCAGCGCCCGC 5681
QY 1852 aSerHisSerHisAlaHisGlnHisSerProLleSerProArgThrGlnAspAlaLeuG 1872
DB 5682 CTCCCATCTCCATGCCACCGACCTCGCCCATCTCCCTCGGACCCAGGATGCCCTCCA 5741
QY 1872 nGlnArgProSerValLeuHisAsnThrGlyMetLysGlyIleThrAlaValGluPr 1892
DB 5742 GCAGAGACCCAGTGTGCTTACAAACACAGGCGATGAAGGGGTATCATCCCGCTGTGAGCC 5801
QY 1892 oSerLysProThrValLeuArgSerThrThrSerSerProValArgProAlaAlaTh 1912

DB 5802 CAGCAAGCCACAGCTGCTGAGGTCCACCTCCACCTCCACCTCCCGGTTCCCGCAGCTGCCAC 5861
QY 1912 rPheProProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyrProThrLe 1932
DB 5862 ATTCCCACTGCGCACCCACCTGCGGCGACCTCGATGGGGTCTATCCCTACCT 5921
QY 1932 uMetGluProValLeuLeuProLysGluAlaProArgValAlaAlaArgProGluArgProAr 1952
DB 5922 CATGGAGCCGCTTCTGCTGCCAAGAGAGGCCCGCGGTCGCGCGGCGAGCGGCCCG 5981
QY 1952 gAlaAspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluProAl 1972
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QY 2032 rIleGlnGluLeuGluLeuArgSerLeuGlyTyrHisGlySerTyrTyrSerProGluG 2052
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DB 6762 GTCGGTCTTGGGTGGTGGAGACGGTATGAACTGTGTCTCCCGGAGGAGCATGAC 6821
QY 2232 rGluProGlyHisSerArgSerAlaValTyrProLeuLeuTyrArgAspGlyGluGlnTh 2252
DB 6822 GAGAGCAGGGCATCTCCCGGAGTCTGTGTACCGCTGCTGTACCGGATGGGAGACAGAC 6881
QY 2252 rGluProSerArgMetGlySerLysSerProGlyAsnThrSerGlnProProAlaPhePh 2272

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6882 GGAGCCAGCAGGATGGGCTCCAGTCTCCAGGCAACACCCAGCCAGCCGCGCTTCTT 6941
2272 eSerLysLeuThrGluSerAsnSerAlaMetValLysLysLysGlnGluLeuAsnLys 2292
6942 CAGCAAGCTGACGAGAGCACTCCGCCATGTCAAGTCCAGAGCAAGAGATCAACA 7001
2292 sLysLeuAsnThrHisAsnArgAsnGluProGluTyrAsnLysSerGlnProGlyThrG 2312
7002 GAGCTGACACCCACACCGGAATGAGCTGAATACAAATATCAGCCAGCTGGACCGA 7061
2312 uilePheAsnMetProAlaIleThrGlyThrGlyLysMetThrTyrArgSerGlnAlaVa 2332
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2332 lGlnGluHisAlaSerThrAsnMetGlyLeuGluAlaIleLysArgLysAlaLeuMetG 2352
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2352 YLysTyrAspGlnTrpGluSerProProLeuSerAlaAsnAlaPheAsnProLeuAs 2372
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2372 nAlaSerAlaSerLeuProAlaAlaMetProIleThrAlaAlaAspGlyArgSerAsp 2392
7242 TGCCAGTGCCAGGCTGCCCGCTGCTATGCCCATACCGCTGCTGACGAGGAGTGA 7301
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7301 CACACTCACCTCGCAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7361
2412 gLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgProSerValSerSe 2432
7362 AAAAGCCAAAGTCCCGCGCGCTGGCATCTGGGAGCGGCGCCACTCTGTCTCTTC 7421
2432 rValHisSerGluGlyAspCysAsnArgArgThrProLeuThrAsnArgValTrpGluAs 2452
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2452 pArgProSerAlaGlySerThrProPheProTyrAsnProLeuIleMetArgLeuG 2472
7482 CAGGCGCTCGTCCGAGGATTCACGCCATTCCTCCATACACCCCTGATCATGCGGCTG 7541
2472 nAlaGlyValMetAlaSerProProProGlyLeuProAlaGlySerGlyProLeuAl 2492
7542 GCGCGGTGTATGGCTTCCCAACCCCGGCGCTCCCGCGGCGAGCGGCGCGCTCGC 7601
2492 aGlyProHisAlaTrpAspGluGluProLysProLeuLeuLysSerGlnTyrGluTh 2512
7602 TGGCCCCCACCACCGCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 7661
2512 rLeuSerAspSerGlu 2517
7662 ACTCTCCGACGAGGAG 7677

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RESULT 7
US-09-819-104A-6
; Sequence 6, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 7386
; TYPE: DNA
; ORGANISM: Mus musculus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(7386)
US-09-819-104A-6
Alignment Scores:
Pred. No.: 0 Length: 7386
Score: 10832.50 Matches: 2149
Percent Similarity: 87.94% Conservatives: 90
Best Local Similarity: 84.41% Mismatches: 197
Query Match: 81.97% Indels: 117
DB: 10 Gaps: 33
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QY 61 ProGlnArgArgArgProSerLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
DB 181 CCACAGAGAGGCGGCCCTCTCTGTCTCAGAGTTCACAGCTGGAGGTGAACGGTCTCAG 240
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
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QY 101 GluPheIleGluSerLysArgProArgGluLeuLeuLeuProAspProLeuLeuArgPro 120
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QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
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QY 141 LeuThrGlyLysLeuGluProValSerProProSerProProHisThrAspProGluLeu 160
DB 421 CTGGCAGGCAAGCTGGAGCTGTGTACCTCCAGTCCCGCAGCTGACCTGAGCTA 480
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAsn---MetAspArgVal 179
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QY 180 AspArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGln 199
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Qy ArgLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgProProSerValSer 2431
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Qy SerValHisSerGluGlyAspCysAenArgAtqThrProLeuThrAenArgValTrpGlu 2451
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Db 7189 GACCGGCCCTCATCTGCAGGGTCCACGCCATCTCCCTACAACTTTGATTATGAGGCTA 7248
2472 GlnAlaGlyValMetAlaSerProProProGlyLeuProAlaGlySerGlyProLeu 2491
Db 7249 CAGCGAGGTGTATGCGCTCCCGGCCACCTGGCCCTTGGCGCAGGAGCGGGCCCCCTA 7308
2492 AlaGlyProHisAlaTrpAspGluGluProLysProLeuLeuCysSerGlnTyrGlu 2511
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2512 ThrLeuSerAspSerGlu 2517
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US-09-819-104A-4
; Sequence 4, Application US/09819104A
; Publication No. US20030027137A1
; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES
; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8544
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)..(7545)
US-09-819-104A-4
Alignment Scores:
Pred. No.: 0 Length: 8544
Score: 10832.50 Matches: 2149
Percent Similarity: 87.94% Conservative: 90
Best Local Similarity: 84.41% Mismatches: 197
Query Match: 81.97% Indels: 117
DB: 10 Gaps: 33
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QY 21 ProHisSerLeuSerTyrProValGlnIleAlaArgThrHisThrAspValGlyLeuLeu 40
Db 220 CCCCATGGCATCTCTACCTCCGTCGAGATAGCCGCTCCCAACAGCGAGTGGCGTGTCT 279
QY 41 GluTyrGlnHisHisSerArgAspTyrAlaSerHisLeuSerProGlySerIleIleGln 60
Db 280 GAGTACCAACACACCCCGTCGACTACACCTCACACCTGTCTACCCCGTTCATCATCAG 339
QY 61 ProGlnArgArgProSerLeuLeuSerGluPheGlnProGlyAsnGluArgSerGln 80
Db 340 CCACAGAGAGGCGGCCCTCACTGTCTCAGAGTTCAGAGTTCAGCTGGGAGTGAACCGTCTCAG 399
QY 81 GluLeuHisLeuArgProGluSerHisSerTyrLeuProGluLeuGlyLysSerGluMet 100
Db 400 GAGCTCCACCTGGCGCCTGAGTCCCGCAGCTTCTGCTGCTCAGAGTTCAGCTGGGAGTGAACCGTCTCAG 399
QY 101 GluPheIleGluSerLysArgProArgLeuGluLeuLeuProAspProLeuLeuArgPro 120
Db 460 GAATTCACCGAGAGCAGCGCCCCCGCTGGAGCTACTACCCGATACCTCTGCTGGCCCA 519

QY 121 SerProLeuLeuAlaThrGlyGlnProAlaGlySerGluAspLeuThrLysAspArgSer 140
Db 520 TCACCCCTGTGTGCCACTTGGGACGCGAGTGGGTCTGAGACCTTTACCAAGACCGGTAGC 579
QY 141 LeuThrGlyLysLeuGluProValSerProProSerProHisThrAspProGluLeu 160
Db 580 CTGGCAGGCAAGCTGGAGCCTGTGTCACTCCAGGTCCCGCCGACGCTACCTGAGCTA 639
QY 161 GluLeuValProProArgLeuSerLysGluGluLeuIleGlnAsn---MetAspArgVal 179
Db 640 GAGCTGGCGGCATCTCGACTGTCCAAGGAGAGCTGATCCAGAACAGATTTGGACCGCGTG 699
QY 180 AspArgGluIleThrMetValGluGlnGlnIleSerLysLeuLysLysGlnGlnGln 199
Db 700 GACCTGAGATCACCATGTTAGAGCAGCAGATCTCCAAGCTGAAGAAGACGACGACACAG 759
QY 200 LeuGluGluAlaAlaLysProGluProGluLysProValSerProProProIle 219
Db 760 TTGAGGAGGAGGCGCGCAAGCCCGCAACCCGAGAAAGCCTGTGTCCGCCACCCCATTA 819
QY 220 GluSerLysHisArgSerLeuValGlnIleIleTyrAspGluAsnArgLysLysAlaGlu 239
Db 820 GAATCAAGACCCGAGCCCTGTGTCCAGATCATCTACGATGAGAACCCGGAAGAAGCGCAA 879
QY 240 AlaAlaHisArgIleLeuGluGlyLeuGlyProGlnValGluLeuProLeuTyrAsnGln 259
Db 880 GCCGCACACCCGATCTTAGAAGGCTTGGGCGCCCGAGGTGGAGCTGCTCTGTACACAG 939
QY 260 ProSerAspThrArgGlnTyrHisGluAsnIleLysIleAsnGlnIleAlaMetArgLysLys 279
Db 940 CCGTCTGACACACCGCCAGTACCATGAAAAATCAAAATTAACACGAGCGATGCGGAAGAAG 999
QY 280 LeuIleLeuTyrPheLysArgArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCys 299
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QY 300 GlnArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGluArgIleGluAsnAsn 319
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QY 320 ProArgArgArgAlaLysGluSerLysValArgGluTyrTyrGluLysGlnPheProGlu 339
Db 1120 CCGCGAAGGAGGCGCCCAAGGAGAGCAAGGTGAGGGAGTACTACGAGAAACAGTTCCCGGAG 1179
QY 340 IleArgLysGlnArgGluLeuGlnArgMetGlnSerArgValGlyGlnArgGlySer 359
Db 1180 ATCCGCAAGCAGCGGAGCTGCAGAGCGCATGCGAGCGGTGGCGAGCGTGGCAGT 1239
QY 360 GlyLeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIleIleAspGlyLeu 379
Db 1240 GGCTCTCCATGTGGCTGCCCGCAGTGAGCATGAGGTTTCTGAGATCATTCATGCGCTTG 1299
QY 380 SerGluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaValIleProProMetLeu 399
Db 1300 TCTGACGAGAGAACTCTGAGAAAGCAGATGCGCCAGCTGCGCGTATCC -GCCATGTTG 1357
QY 400 TyrAspAlaAspGlnGlnArgIleLysPheIleAsnMetAsnGlyLeuMetAlaAspPro 419
Db 1358 TACGACGC -GACCAGCAGAGGATCAAGTTTCATCACTCACTGAATGGACTCATGATGACCCC 1416
QY 420 MetLysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGlnGluLysGluThr 439
Db 1417 ATGAGGTCTACAAGACCGCTCAGGTTTACCAATGTGGAGGAGCAGAGAGGAGCACCC 1476
QY 440 PheArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIleAlaSerPheLeuGlu 459
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QY 480 LysSerLeuValArgArgSerTyrArgArgArgGlyLysSerGlnGlnGlnGlnGln 499
DB 1597 AAGAGCTTGCTGAGCGGAGCTATCGCGCCGTGGCAAGAGCAGCAGCAGCAGCAG 1656
QY 500 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 519
DB 1657 CAACACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1704
QY 520 LysAspGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLys 539
DB 1705 AAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1764
QY 540 AsnAspLysGluAspLeuLysGluLysGluLysGluLysGluLysGluLysGlu 559
DB 1765 AACGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1824
QY 560 GluLysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSerGlnGlyArgGly 579
DB 1825 GAGAAAGAGCGCTGCCCTCCAAAGGCCGCAAACTGCCCAAGCCGCGCGCAAA 1884
QY 580 GlyArgLysThrArgSerMetAlaAsnGluAlaAsnSerGluLysAlaLysThrProGln 599
DB 1885 GGCCTGATCAGCGCTCCATGTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1944
QY 600 GlnSerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArgTrpThrGluGlu 619
DB 1945 CAAAGTTGAGAGCTGGCTTCCATGGAGATGCAACGAGAGTCTCGCTGGACTGAGGAAGAG 2004
QY 620 MetGluThrAlaLysLysGlyLeuLeuGluHisGlyArgAsnTrpSerAlaLysAlaArg 639
DB 2005 ATGGAGACAGCAAGAAAGAGCTCTCGGAACATGGGAGGAGTGTGTCAGCCATTGCCCGC 2064
QY 640 MetValGlySerLysThrValSerGlnCysLysAsnPheTyrPheAsnTrpLysLysArg 659
DB 2065 ATGGTGGCTCAAGACCGTGTCCCGAGTGTAGAACTTCTACTTCACTACAGAGAGAGG 2124
QY 660 GlnAsnLeuAspGluLeuGlnGlnHisLysLeuLysMetGluLysGluArgAsnAla 679
DB 2125 CAGAACCTGGACGAAATCTTCAGCAGCAGCAGCAGTAAAGATGAGAGGAGGAGGAGCT 2184
QY 680 ArgArgLysLysLysLysAlaProAlaAlaLysSerGluLysAlaLysPheProVal 699
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QY 700 ValGluAspGluGluMetGluAlaSerGlyValSerGlyAsnGluGluMetValGlu 719
DB 2245 GCTGAGGACAGAGATGAGAGATCAGCGGAGGAGTCCCATGAGAGAGAGGAGTGGCGAG 2304
QY 720 GluAlaGluAlaLeuHisAlaSerGlyAsnGluValProArg---GlyGluCysSerGly 738
DB 2305 GAGGCAAGAGCTCACAGGCTCTGGGATGAGTTCCAGAGTTGGGAGTGCAGTGGC 2364
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QY 759 AlaLysAspThrGlyGlnAsnGlyProLysProProAlaThr---LeuGlyAlaAsp 776
DB 2425 ACGAGGACACT-----GGGCTTAACCCACTGGGACTGAGCATGCGCGTGGC 2475
QY 777 GlyProProGlyProProThrProProArgArgThrSerArgAlaProLysGluPro 796
DB 2476 ACCGACCACTGTTCTCT-----CTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 2529
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DB 2530 TCCCCAGTCCCTGATGCCAGTGGCCCACTATCCCAAGAGCTTCC---CCATCAGCTGCC 2586
QY 817 AlaProProValValProLysGluGluLysGluGluThrAlaAlaAlaProPro 836
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QY 837 ValGluGluGlyGluGluGlnLysProProAlaAlaGluGluAlaValAspThrGly 856

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QY 1138 SerGluHisAlaLysAlaProValGlyProValThrMetGlyLeuProProMetAsp 1157
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 1694 GlnMetHisHisAsnThrAlaThrAlaMetAlaGlnArgAlaAspMetLeuArgGlyLeu 1713
 5131 CAGATGCAACCAACAGCTGCTCCGCCATGCCCAGCGTGTGACATGCTGAGGGGTCTG 5190
 1714 SerProArgGluSerSerLeuAlaLeuAsnTyrAlaAlaGlyProArgGlyIleIleAsp 1733
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 1854 HisSerHisAlaHisGlnHisSerProIleSerProArgThrGlnAspAlaLeuGln 1873
 5569 CACACC-----CACAGCACTCGCCATCTCCCGCGGACCCAGACCGCTTGCAGCAG 5622
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Qy	1914	ProProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyrProThrLeuMet	1933
Db	5743	CCACCTGCGACCCACTGCGCACTTGGTGGCACCCCTTGAAGGGGTCTACCTCATCCCTCATG	5802
Qy	1934	GluProValLeuLeuProLysGluAlaProArgValAlaArgProGluAlaArgProAla	1953
Db	5803	GAGCCCGTCTGTATACCCAGAGACCTCTCGGGTCGCCCGCCGAGCGCCCGGTGTG	5862
Qy	1954	AspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluProAlaSer	1973
Db	5863	GACGGTGGCCATGCTTCTTCCACCAACCCCGGCCCGG-----GAGCCCGCTCC	5913
Qy	1974	SerProSerLysGlySerGluProArgProLeuValProProValSerGlyHisAlaThr	1993
Db	5914	TCACCCAGCAGAGCTCCGAGCCCGCATCCCTAGCACCCCGCCAGCTCCAGCCACACAGCC	5973
Qy	1994	IleAlaArgThrProAlaLysAsnLeuAlaProHisHisAlaSerProAspProAla	2013
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Qy	2014	ProProAlaSerAlaSerAspProHisArgGluLysThrGlnSerLysProPheSerIle	2033
Db	6034	--CCACCTCGGCCTCAGATCTGCACCGAGAAAGACTCAAAGTAACCTTTTCCATC	6090
Qy	2034	GlnGluLeuGluLeuArgSerLeuGlyTyrHis---GlySerSerTyrSerProGluGly	2052
Db	6091	CAGAAATTGGAACCTCCGTTCTCTGGGTATACCACAGTGGAGCTGCTGTACAGCCCGTGG	6150
Qy	2053	ValGluProValSerProValSerSerProSerLeuThrHisAspLysGlyLeuProLys	2072
Db	6151	GTGAGGCCCATCAGCCCGGTGAGCTCCCCAGCTGTACCCACGACAAAGGGGCTCTCCAA	6210
Qy	2073	HisLeuGluGluLeuAspLysSerHisLeuGluGlyGluLeuArgProLysGlnProGly	2092
Db	6211	CCTCTGGAGAGCTAGAGAGAGCCACTTGGAGGGGAGCTGCGGCACAGCAGCCAGGC	6270
Qy	2093	ProValLysLeuGlyGlyGluAlaHisLeuProHisLeuArgProLeuProGluSer	2112
Db	6271	CCCATGAAGCTCAGCGGGAGGCTGCCCATCTCCACATCTGCGGCCACTGCCCGAGAGC	6330
Qy	2113	GlnProSerSerProLeuLeuGlnThrAlaProGlyValLysGlyHisGlnArgVal	2132
Db	6331	CAGCCCTCATCCAGCCCACTCTCTCCAGACTGCCCGGGCATCAAAGGTCAACAGAGGGT	6390
Qy	2133	ValThrLeuAlaGlnHisIleSerGluValIleThrGlnAspTyrThrArgHisHisPro	2152
Db	6391	GTACCCCTGGCTAGCAGCATCAGCGAGGTCAATTACGAGAGACTACACCCGGCACCCCG	6450
Qy	2153	GlnGlnLeuSerAlaProLeuProAlaProLeuTyrSerPheProGlyAlaSerCysPro	2172
Db	6451	CAGCAGCTCAGTGGCCCTCTCCCGCCCTCTCTACTCTTTCGCGAGCCAGCTGCCCT	6510
Qy	2173	ValLeuAspLeuArgArgProProSerAspLeuTyrLeuProProProAspHisGlyAla	2192
Db	6511	GTGCTGATCTTCCCGCGCCACCCAGTGAACCTCTTACTTCCACCCCGACCATGGCACC	6570
Qy	2193	ProAlaArgGlySerProHisSerGluGlyGlyLysArgSerProGluProAsnLysThr	2212
Db	6571	CCAGCCCGGGATCCCCCAACAGTGAAGGGGGCAAAAGGTCCCAGAAACCCAGCAAAACA	6630
Qy	2213	SerValLeuGlyGlyGluAspGlyIleGluProValSerProProGluGlyMetThr	2232
Db	6631	TCGGTCTGGGCAGCAGTGAGGATGCCATTGAGCCTGTGTCCCCACAGAGGGCATGACT	6690
Qy	2233	GluProGlyHisSerArgSerAlaValTyrProLeuLeuTyrArgAspGlyGluGlnThr	2252
Db	6691	GAGCCAGGACATGCTCGAGCGCGCTGTGTATCCCATCTGTATCGAGACGGGAAACAGGC	6750
Qy	2253	GluProSerArgMetGlySerLysSerProGlyAsnThrSerGlnProProAlaPhePhe	2272
Db	6751	GAGCCC---AGGATGGGCTCTAAGTCTCCAGGGCAACACAGCCAGCCGCGCCAGCTTCTTC	6807
Qy	2273	SerLysLeuThrGluSerAsnSerAlaMetValLysSerLysLysGlnGluIleAsnLys	2292

Db	6808	AGTAAAGCTGACTGAGACCAACTCGCCATCGTGAAGTCGAAGAAGCAGAGAGATCAACCAAG	6867
Qy	2293	LysLeuAsnThrHisAsnArgAsnGluProGluTyrAsnIleSerGlnProGlyThrGlu	2312
Db	6868	AAACTCAACACCACACCGGAAGCAGCCAGATACAAATATGGCCAGACCTGGGACGGAA	6927
Qy	2313	IlePheAsnMetProAlaIleThrGlyThrGlyLeuMetThrTyrArgSerGlnAlaVal	2332
Db	6928	ATCTTCAACATGCCCGCCATCACTGGAGCAGCGCTTATGACCTGTAGAACGCCAGCGCGTG	6987
Qy	2333	GlnGluHisAlaSerThrAsnMetGlyLeuGluAlaIleIleArgIleAlaLeuMetGly	2352
Db	6988	CAGAACACGCCAGCACCAACATGGGCTAGAGCCCAATTATTAAAGGCACCTCATGGGT	7047
Qy	2353	LysTyrAspGlnTrpGluGluSerProProLeuSerAlaAsnAlaPheAsnProLeuAsn	2372
Db	7048	AAATATCATCAGTGGGAAGAGCCCGCCGCTCGGCGCCAATGCTTTTAAACCTCTGAAT	7107
Qy	2373	AlaSerAlaSerLeuPro----AlaAlaMetProIleThrAlaAlaAspGlyArgSerAsp	2391
Db	7108	GCCAGCGCCAGTCTGCCCGCTGCTGCTATGCCATAACCACTGCTGACGACGGAGTGAC	7167
Qy	2392	HisThrLeuThrSerProGlyGlyGlyLeuAlaLysValSerGlyArgProSerSer	2411
Db	7168	CAGCATCTACCTGCCAGGTGGAGGTGGGAAGCCAAAGTCTCTGCGACACCTAGGACG	7227
Qy	2412	ArgLysAlaLysSerProAlaProGlyLeuAlaSerGlyAspArgProProSerValSer	2431
Db	7228	CGAAAGCCCAAGTCGCCAGCACCAAGGCTAGCGTCGGAGACCGACCCCTTCTGTCTCC	7287
Qy	2432	SerValHisSerGluGlyAspCysAsnArgArgThrProLeuThrAsnArgValTrpGlu	2451
Db	7288	TCAGTACACTAGAGGGGGAGCTGCAATCGCGCAACACCACTCACCAACCCGTGTGGGAG	7347
Qy	2452	AspArgProSerSerAlaGlySerThrProPheProTyrAsnProLeuIleMetArgLeu	2471
Db	7348	GACCGGCCCTCATCTGCAGGGTCCACGCCAATTCCTTACAAACCTTTGATTATGAGGCTA	7407
Qy	2472	GlnAlaGlyValMetAlaSerProProProProGlyLeuProAlaGlySerGlyProLeu	2491
Db	7408	CAGCGCAGGTGTCAATGGCTCTCCCGCCGCCACCTTGGCCCTTCGGCGAGCAGCGGCCCTA	7467
Qy	2492	AlaGlyProHisAlaTrpAspGluProLysProLeuLeuCysSerGlnTyrGlu	2511
Db	7468	GCTGGTCCCCACACCGCTGGATGAGAGCCCAAGCCACTGCTGTGTTCACAGTATGAG	7527
Qy	2512	ThrLeuSerAspSerGlu	2517
Db	7528	ACACTCTCGACACGCGAG	7545

RESULT 9

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RESULDI 9
US-10-087-192-650
; Sequence 650, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 650
; LENGTH: 7534
; TYPE: DNA
; ORGANISM: Mus musculus

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US-10-087-192-650

Alignment Scores:
Pred. No.: 0 Length: 7534
Score: 9691.50 Matches: 1893
Percent Similarity: 87.70% Conservatives: 82
Best Local Similarity: 84.06% Mismatches: 171
Query Match: 73.34% Indels: 106
Gaps: 28

US-09-522-753-5 (1-2517) x US-10-087-192-650 (1-7534)

QY 295 LysGlnLysPheCysGlnArgTyrAspGlnLeuMetGluAlaLeuGluLysLysValGlu 314
DB 2 GAACAGCGCTTCTGCGAGCGCTATGACAGCTCATGGAGCGCTGGAGAGAGAGTAGAG 61
QY 315 ArgIleGluAsnAsnProArgArgAlaLysGluSerLysValArgGluTyrValGlu 334
DB 62 CGCATAGAGAACAAATCCGGAAGGAGGCGCAAGGAGCAGAGTGGAGGAGTACTACGAG 121
QY 335 LysGlnPheProGluIleArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgVal 354
DB 122 AAACAGTTCCTCGAGATCCGCAAGCAGCGGAGCTGCAGAGCGCATGCAGAGCGAGGTG 181
QY 355 GlyGlnArgGlySerGlyLeuSerMetSerAlaAlaArgSerGluHisGluValSerGlu 374
DB 182 GGCAGCGCTGGCAGTGGCTCTCCATGTGCGCTGCGCGCAGTGGAGTCTGAG 241
QY 375 IleLeuAspGlyLeuSerGluGlnGluAsnLeuGluLysGlnMetArgGlnLeuAlaVal 394
DB 242 ATCATGATGGCTGTGCTGAGCAGGAGAACCTCGAGAGCAGATGCGCAGCTGGCGGTG 301
QY 395 IleProProMetLeuTyrAspAlaAspGlnGlnArgLysPheIleAsnMetAsnGly 414
DB 302 ATCCCGCCCATGTTGACGAGCGGACAGCAGAGGATCAAGTTCAACATGAATGGA 361
QY 415 LeuMetAlaAspProMetLysValTyrLysAspArgGlnValMetAsnMetTyrSerGlu 434
DB 362 CTCATGATGATGACCCATGAGGCTCTCAAGAGCCGTGAGTTACCAACATGTGAGCGGAG 421
QY 435 GlnGluLysGluThrPheArgGluLysPheMetGlnHisProLysAsnPheGlyLeuIle 454
DB 422 CAGGAGGGGACACCTTCCTGAGAGTATATGAGCAGCAGCCTTAAGAACTTTGCGCTGAT 481
QY 455 AlaSerPheLeuGluArgLysThrValAlaGluCysValLeuTyrTyrLeuThrLys 474
DB 482 GCCTCATCTCTGGAGAGAAAGCGTCTGAGTGTCTCTATTAATCTACTGACCAAG 541
QY 475 LysAsnGluAsnTyrLysSerLeuValArgArgSerTyrArgArgArgGlyLysSerGln 494
DB 542 AAGAAATGAAATTAACAGAGCTTGTGAGCGGAGCTATCGGCGCGCGAGAGCCAG 601
QY 495 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 514
DB 602 CAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 649
QY 515 SerSerGlnGlnGluLysAspGluLysGluLysGluLysGluAlaGluLysGluGlu 534
DB 650 AGCAGCCAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 709
QY 535 LysProGluValGluAsnAspLysGluAspLeuLeuLysGluLysThrAspAspThrSer 554
DB 710 AAGCAGGATGCGAGAACAGAGAGAGAGAACTCAGCAGGAGAGAGAGAGAGAGAGAG 769
QY 555 GlyGluAspAsnAspGluLysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSer 574
DB 770 GCGCAGGACACAGATGAGAGAGAGCGCTGGCTCCAAAGGCGCGCAAACTGCCAACAGC 829
QY 575 GlnGlyArgArgLysGlyArgGlyLeuThrArgSerMetAlaAsnGluAlaAsnSerGlu 594
DB 830 CAAGCGCCCGCAAGAGCGCTATCAGCGCTCATGCGCAACAGCGCCCAACATGAGGAG 889
QY 595 AlaIleThrProGlnGlnSerAlaGluLeuAlaSerMetGluLeuAsnGluSerSerArg 614

DB 890 ACAGCCACCCACAGCAAGTTCCAGAGCTGGCTTCCATGAGATGAACAGAGATTCCTCGC 949
QY 615 TrpThrGluGluMetGluThrAlaLysLysLysGlyLeuLeuGluHisGlyArgAsnTyr 634
DB 950 TGGACTGAGGAAGAGATGGAGCAGCAAGAAAGAGGCTCTCGAAACATGGAGGAACTGG 1009
QY 635 SerAlaIleAlaArgMetValGlySerLysThrValSerGlnCysLysAsnPheTyrPhe 654
DB 1010 TCAGCCATTGCCCGCATGTGGCTCCAGACCGTGTCCAGTGAAGAACTTCTACTTC 1069
QY 655 AsnTyrLysLysArgGlnAsnLeuAspGluIleLeuGlnGlnHisLysLysLeuLysMetGlu 674
DB 1070 AACTACAAGAGAGCGCAACCTGGACGAATCTTCAGCAGCAGCAAGCTAAAGATGGAG 1129
QY 675 LysGluArgAsnAlaArgArgLysLysLysAlaProAlaAlaAlaSerGluGluAla 694
DB 1130 AAGAGAGGAAACGCTCGAGGAAAGAAAGAACCCAGCTCGGCGAGCGGAGGAGACA 1189
QY 695 AlaPheProValValGluAspGluMetGluAlaSerGlyValSerGlyAsnGlu 714
DB 1190 GCCTTCCACCTGCGCTGAGCAGAGAGATGAAGCATCAGGCGCAAGTGCACATGAG 1249
QY 715 GluGluMetValGluGluAlaGluAlaLeuHisAlaSerGlyAsnGluValProArg 733
DB 1250 GAAGAGCTGGCGGAGGAGGAGAGAGCTCACAGGCTCTGGGAATGAGTTCCAGAGTT 1309
QY 734 GlyGluCysSerGlyProAlaThrValAsnAsnSerSerAspThrGluSerIleProSer 753
DB 1310 GGGAGTGCATGGCCCGAGCTGCTGCTCAACAACAGCTCTGATCTAGAGTGTCCATCC 1369
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DB 1370 CCGCTTTCAGAGGCGCAGCAAGGACACT-----GGGCTTAAACCCCTGGCACTGAA 1420
QY 773 LeuGlyAlaAspGlyProProGlyProProThrProProArgArgThrSerArg 791
DB 1421 GCATTGCGCGCTGCCACCCAGCGCTTCTCT-----CTCCAGAGAACCGGACCA 1474
QY 792 AlaProIleGluProThrProAlaSerGluAlaThrGlyAlaProThrProProAla 811
DB 1475 GCGCTGTGTGAGCTCTCCAGTCTCTGATGCGAGTGGCGCCACCATCCCGAGCTTCC 1534
QY 812 ProProSerProSerAlaProProValProLysGluGluLysGluGluGluThr 831
DB 1535 ---CCATCACCTGCGCGACCCCGCTACTGTGGCAAGAGTGAACAAGAGCCCGCGCT 1591
QY 832 AlaAlaAlaProValGluGluGlyGluGluGlnLysProProAlaAlaGluLeu 851
DB 1592 GCTTCAGCTCCCGCAGCAGAGATGCCAAGGAGCAGAGTCTGAGGCGCGAGGAG-----Val 862
QY 852 AlaValAspThrGlyLysAlaGluPro-----GAGGCGCGAGGAGTGA 1702
DB 1646 ---ATCATGTGGAAAGCCAGAGGAGCGCGCTCTGAGAGCGCGCGAGAGTGA 1702
QY 863 LysSerGlyCysThrGluGluAlaGluGluGlyProAla---LysGlyLysAspAlaGlu 881
DB 1703 AAGAGTGACCAACAGGAGGAGCGCGAGGAGAGCTGAAAGCAAAAGCAAGGCGCAGAG 1762
QY 882 AlaAlaGluAlaThrAlaGluGlyAlaLeuLysAlaGluLysGluGlyGlySerGly 901
DB 1763 GCCATTGAAACTGTGTCTGAGGCGCACCTTAAGTGGAG-----GAGCTGTGTAGCAAG 1816
QY 902 ArgAlaThrThr---AlaLysSerSerGlyAlaProGlnAspSerSerSerAlaThr 920
DB 1817 GCAGCTGTGACCAAGGGTTCAGTGTGCCACCCAGGACAGTACTCCAGTGCACACC 1876
QY 921 CysSerAlaAspGluValAspGluAlaGluGlyGlyAspLysAsnArgLeuLeuSerPro 940
DB 1877 TGCAGTGCGCATGAGTGGAGCGAACCCGAAGGAGGTGACAAGGCGCAGGCTGTGTCCCA 1936
QY 941 ArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSerProGlnLysPro 960

Db 1937 AGGCCACGCTCTCTACCCCGGCTGGAGATCCCGGGCCAGTACTCTCGCCCCAGAACCGC 1996
Qy 961 LeuAspLeuLysGlnLeuLysGlnArgAlaAlaIleProProIleGlnValThrLys 980
Db 1997 CTGGACCTGAAGCAGCTGAAGCAGGAGCAGCGCCCATCCCCCTATC---GTCAACCAAG 2053
Qy 981 ValHisGluProProArgGluAspAlaAAlaProThrLysProAlaProProAlaProPro 1000
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Qy 1001 ProProGlnAsnLeuGlnProGluSerAspAlaProGlnGlnProGlySerSerProArg 1020
Db 2114 CCACGACGACCTTACAGCCAGAGGGTGAGTGCTCAGCAGTCGGGAGGAGTCCACGT 2173
Qy 1021 GlyLysSerArgSerProAlaProProAlaAspLysGlu----- 1033
Db 2174 GGCAAGTCCCGCAGCCAGTGCCTCTCCGAGAAAGAGCAGAAACCCGCACTCTTT 2233
Qy 1034 ---AlaPheAlaAlaGluAlaGlnLysLeuProGlyAspProProCysTrpThrSerGly 1052
Db 2234 CCGGCTTTCCTCACTGAGGGCCCAAGACTACCGACTGAGCCCCCAGCGCTGTCATCGGC 2293
Qy 1053 LeuProPheProValProProArgGluValIleLysAlaSerProHisAlaProAspPro 1072
Db 2294 CTGCCCTTCCCCATCTCCACGGGAGGTGATCAAGACTTCCCCACACCGCGCTGACCCC 2353
Qy 1073 SerAlaPheSerTrAlaProProGlyHisProLeuProLeuGlyLeuHisAspThrAla 1092
Db 2354 TCTGCCCTTCTCTACACACCCCGGTCACCGCTGCTCTGGGCTTCCAGTAGTGCC 2413
Qy 1093 ArgProValLeuProArgProProThrIleSerAsnProProProLeuIleSerSerAla 1112
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Qy 1113 LysHisProSerValLeuGluAlaArgGlnIleGlyAlaIleSerGlnGlyMetSerValGln 1132
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Qy 1153 ProLeuProMetAspProLysLysLeuAlaProPheSerGlyValLysGlnGluLeu 1172
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Qy 1173 SerProArgGlyGlnAlaGlyProProGluSerLeuGlyValProThrAlaGlnGluAla 1192
Db 2617 ----- 2617
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Qy 1213 ProSerThrArgValProSerAspSerAlaIleThrTrpArgGlySerIleThrHisGly 1232
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Db 2780 AGTCGCTTACCGGACAGAGGACACCCCTCGCCCAAGGGCCATGTCATCTATGAGGGC 2839
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Qy 1333 ArgAlaIleProProGluArgHisSerProHisHisLeuLysGluGlnHisHisIleArg 1352
Db 3020 CGGCGCATC---CCTGAGCAGCACAGCCCC---CACCTCAAGGAGCAGCATCATACCGA 3073
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Qy 1393 LeuThrGluAlaTrpLysThrGln-----AlaLeuGlyProLeuLysLeuLysPro 1409
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Qy 1410 AlaHisGluGlyLeuValAlaThrValLysGluAlaGlyArgSerIleHisGluIlePro 1429
Db 3254 ACTCACAGGGGTGTGTAGCAACTGTGAAGAGCGCGCGCTCTATCCATGAGATCCCG 3313
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Qy 1470 LysHisAspValArgSerLeuIleGlySerProGlyArgThrPheProProValHisPro 1489
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Qy 1649 TyrTrpLeuProArgHisLeuAlaProAsnProThrTrpProHisLeuTrpProProTyr 1668
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QY 1669 LeuIleArgGlyTyrProAspThrAlaAlaLeuGluAenArgGlnThrIleIleAsnAsp 1688
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 QY 1829 ProGlyThrGluGlnSerSerGlySerSerGlySerSerGlyGlyGlyGlySerSer 1848
 DB 4496 CTTGTTACGAGCAGACGCGGGCT-----GGGGGCGAG 4531
 QY 1849 SerArgProAlaSerHisSerHisAlaHisGlnHisSerProIleSerProArgThrGln 1868
 DB 4532 AGCGCGCGCGCTCTCCACACC-----CACAGCATTGCGCCATCTCCCGCGGACCCAG 4585
 QY 1869 AspAlaLeuGlnGlnArgProSerValLeuHisAsnThrGlyMetLysGlyIleIleThr 1888
 DB 4586 GACCGCTTGACGAGAGCGCCAGTGTCTGCACAAACAGGACATGAAGGCGGTGGTCACC 4645
 QY 1889 Ala-ValGluProSerLysProThrValLeuArgSerThrSerThrSerSerProValAr 1908
 DB 4646 TCCCGTGGAAACCGGCGACGCGCCAGTGTCTGCACAAACAGGACATGAAGGCGGT 4705
 QY 1908 gProAlaAlaThrPheProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyWa 1928
 DB 4706 CCCAGCTGCCACATTCACCTGCGCCACCCACTGCGCCACTTGGTGCCACCTTGAAGGGGT 4765
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 DB 4766 CTACCTACCTCATCGAGCGCGCTCTGTACCCCAAGGAGACCTCTCGGTGCGCGCGCC 4825
 QY 1948 oGluArgProArgAlaAspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGl 1968
 DB 4826 CGAGCGCGCGGTGTGAGCGGTGCGCATGCTTCTTACCAAAACCCCGCGCGCG----- 4880
 QY 1968 yLeuGluProAlaSerProSerLysGlySerGluProArgProLeuValProProVa 1988
 DB 4881 ----GAGCGCGCTCTCTACCCAGCAGAGTCCGAGCGCGCATCCCTTAGCACCCCGCCAG 4936
 QY 1988 lSerGlyHisAlaThrIleAlaArgThrProAlaLysAsnLeuAlaProHisHisAlaSe 2008
 DB 4937 CTCCAGCCACACAGCCATTCGCGCGCACCCAGCAAGAGCGCTTGACCCCAACCATGCCAG 4996
 QY 2008 rProAspProAlaProProAlaSerAlaSerAspProHisArgGluLysThrGlnSe 2028
 DB 4997 TCCGAGACCGCGCGG-----CCACCTCGCGCTCAGATCTGCACCCAGAAAAGACTCAAAG 5053
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 DB 5114 CTACAGCCCGATGGGTGGAGCCCATCAGCCGGTGAAGTCCCGGAGCTGACCCACGCA 5173
 QY 2067 pLysGlyLeuProLysHisLeuGluLeuAspLysSerHisLeuGluGlyGluLeuAr 2087
 DB 5174 CAAGGGGCTCTCCAAACCTCTGGAAGAGCTAGAGAGAGCCACTTGGAGGGGAGCTGCG 5233
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 DB 5951 TAGAGCCAGGCGGTGCAAGNACACCCAGCACCACATACATGGGCTAGAGGCCATATTAG 6010
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 DB 6011 AAAGGCATCATGGTAAATATGATCAGTGGGAAGAGCCCGCGCTCGGCGCCAATGC 6070
 QY 2367 aPheAsnProLeuAsnAlaSerAlaSerLeuPro---AlaAlaMetProIleThrAlaAl 2386
 DB 6071 TTTTAACTCTCTGAATGCCAGCGCCAGCTGTGCCGCTGTGCTATGCCCATTAACCACTGC 6130
 QY 2386 aAspGlyArgSerAspHisThrLeuThrSerProGlyGlyGlyGlyLysAlaLysValSe 2406

Db 243 TTGACCCCACTCCATACACCCCGCGCATCCCTCTGGACGACGCGCTGCTACTACTG 302
Qy ProArgHisLeuAlaProAsnProThrTyrProHisHisLeuTyrProTyrLeuIleArg 1671
Db 303 CCGGACACCTGGCCCAACCCACCTACCGGACCTGTACCCACCTACTACTCCGC 362
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Db 363 GGCTACCCCGACACCGCGGGCTGGAGAACCGGACAGACCATCATCAATGACTACATCACC 422
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Db 423 TCGCAGCAGATGACACCAACCGCGCCACCGCCATGCGCCAGAGCTGATATGCTGAGG 482
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Db 483 GGCTCTCGCCCGCGAGTCTCTGCTGGCACTCACTACGCTGGGGTCCCGAGGCATC 542
Qy IleAspLeuSerGlnValProHisLeuProValLeuValProProThrProGlyThrPro 1751
Db 543 ATCGACCTGTCCCAAGTGCACACCTGCTGTGCTCGTGGCCCGACACAGGACCCCA 602
Qy AlaThrAlaMetAspArgLeuAlaTyrLeuProThrAlaProGlnProPheSerSerArg 1771
Db 603 GCCACCGCCATGGACCGCTTGCCTACTCCCAACCGCGCCACCGCTTTCAGCAGCGC 662
Qy HisSerSerProLeuSerProGlyGlyProThrHisLeuThrLysProThrThrThr 1791
Db 663 CACAGAGCTTCCCACTCTCCCAAGAGGTCCAAACACACTTGACAAACACACACACG 722
Qy SerSerSerGluArgGluArgAspArgAspArgGluArgAspArgGluArgGlu 1811
Db 723 TCCTCGTCCGAGCGGAGCGAGACCGGATCGAGACGGGATCGGAGCGGAA 782
Qy LysSerIleLeuThrSerThrThrThrValGluHisAlaProIleThrArgProGlyThr 1831
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Db 1623 GGCCCGCTGAAGCTTGGCGGGAGGCGGCCACCTCCACACCTGCGCGCGCTGCTGAG 1682
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Db 1743 GTGGTCACTCCGCGGACGACATCAGTGAGTCAACACAGAGTACTACCCGCGCACAC 1802
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Db 1803 CCACAGAGCTCAGCGCACCCCTGCGCGCCCTCTACTCTCTCTGCGCGCAGCTGC 1862
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Db 1863 CCGCTCTCGACCTTCCGCGCCCGCCACCCAGTGAGCTCTACTCTCCGCGCCCGGACCATGT 1922
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Db 1983 ACCTCGCTCTGGGTGGTGGTGGAGCGTATTGAACCTGTGTCCCGACCGCGAGGCGATG 2042
Qy ThrGluProGlyHisSerArgSerAlaValTyrProLeuLeuTyrArgAspGlyGluGln 2251
Db 2043 ACGAGCCAGGGCACTCCCGAGTGTGTGTACCCGCTGTGTACCGGGATGGGGAACAG 2102
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Db 2223 AAGAAGCTGAACCCCAACACCGGAATGAGCTGTATACATATATCAGCCAGCTTGGGACG 2282
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Qy ValGlnGluHisAlaSerThrAsnMetGlyLeuGluAlaIleIleArgLysAlaLeuMet 2351
Db 2343 GTGCAGGAACATGCCAGACCAACATGGGGCTGGAGGCCATATATTAGAAAGGCACTCATG 2402
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Db 2402 ----- 2402


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QY 2421 LeuAlaSerGlyAspArgProProSerValHisSerGluGlyAspCysAsn 2440
Db 7270 TACTTAGGAACAGGAGCGGCTCTTCTGATCTCTCTGATCATTCAGAGGGGATACCAT 7329
QY 2441 ArgArgThrProLeuThrAsnArgValTipGluAspArgProSerSerAlaGlySerThr 2460
Db 7330 AGCAGACGCCA-----GGGTGGGCTGGGAAGACAGGCGCTCTTCAACAGGCTCAACT 7383
QY 2461 ProPheProTyrAsnProLeuLeuMetArgLeuGlnAlaGlyValMetAlaSerProPro 2480
Db 7384 CAGTTTCCTTATAACCTCTGACTATGCGGATG-----CTCAGCAGTACTCCACCA 7434
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Db 7435 ACACCGATTGCGTGTCTCCCTCTGGGTGCAACCAAGCAGCTCTCACCACAGACAGG 7494
QY 2497 AlaTipAspGluGluProLysProLeuLeuCysSerGlnTyrGluThrLeuSerAspSer 2516
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QY 2517 Glu 2517
Db 7555 GAT 7557

RESULT 13
US-10-087-192-649
; Sequence 649, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 649
; LENGTH: 91141
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(91141)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-649

Alignment Scores:
Pred. No.: 4,84e-211 Length: 91141
Score: 3649.00 Matches: 1407
Percent Similarity: 19.86% Conservative: 85
Best Local Similarity: 18.73% Mismatches: 234
Query Match: 27.61% Indels: 5797
DB: 12 Gaps: 57

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Db 57918 GCTGGGCTCCAGCTTCCTCGGAGGACAGCCTAGGACTGTATGGAGGTGATCCGGGAAC 57977
QY 714 GluGluGluMetValGluGluAlaGluAlaLeuHisAlaSerGlyAsnGluValProArg 733
Db 57978 CCTTAGCTGTCACTT-----TCTGTTCCAGG 58004
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Db 58005 -----TCAGGCCAGTA-----TCATTACGGGTGTGTGATTCCCCAG 58040
QY 754 ProHisThrGluAlaAlaLysAspThrGlyGlnAsnGlyProLysProProAlaThrLeu 773
Db 58041 CCAAGGCTT---GCAGCTCAGACAGATGGCAGCTAAAGCCAGAGCTTGTGA--AGCCTC 58095
QY 774 GlyAlaAspGlyProProProGlyProProThrProProArgArgThrSerArgAlaPro 793
Db 58096 AGTCAGTGTGGCTGTCTCTGGGTGTTCACACCT-----GAAAGTCACAGGGGACCT 58149
QY 794 IleGluProThrProAlaSerGluAlaThrGlyAlaProThrProProProAla----- 811
Db 58150 ---GAGCCTTGTGGCAGCAGCCATGGCAGCCATGGGTGGAGCCAGCTGCTCGCGTT 58206
QY 812 -----ProProSerProSerAlaProProAlaProThrProProProAla----- 855
Db 58207 CTCAGTCTCCCTGCATCTCAGCAGCTGGGCGCTCAGTCTTCCCATCTGG--AGGGTGAAG 58265
QY 829 GluGluThrAlaAlaAla-----ProPro 836
Db 58266 GAACAGACTGGCTGTGCATCCGAAACAGTCTACCTTTTCTGTTGTTGGCCCA--- 58322
QY 837 ValGluGluGlyGluGluGlnLysProProAlaAlaGluGluLeuAlaValAspThr--- 855
Db 58323 -----CATGGCTCCAATCCAGACATGCCCATATTTGGCAGGTGCACGAGACCTGA 58376
QY 856 -----GlyLysAlaGluGluProValLysSerGluCysThrGluGluAlaGluGly 873
Db 58377 TCAAAATGGGTCTGGTCACTGTCCT-----CAGTGTACCTTACAGGCTCATCAGGC 58427
QY 874 ProAlaLysGlyLysAspAlaGluAlaThrAlaGluGlyAlaLeuLysAla 893
Db 58428 CCGGCT-----GGAGCTCAGCCTAGT 58448
QY 894 GluLysLysGluGlyGlySerGlyArgAlaThrAlaLysSerSerGlyAlaProGln 913
Db 58449 GACCAG-----TATAGTAGATG--GTTAGCGCACAGACTGCTCTGCCCATGTC 58495
QY 914 AspSerAspSerSerAla-----ThrCysSerAlaAspGluVal 926
Db 58496 TCATCTAGATGACTGCTGCTATTAACCATCCATCCATTGGCAGACGTGCAGC----- 58543
QY 927 AspGluAlaGluGlyAspLysAsnArgLeuLeuSerProArgProSerLeuLeuThr 946
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QY 947 ProThrGlyAspProArgAlaAsnAlaSerProGlnLysProLeuAspLeuLysGlnLeu 966
Db 58580 CCT-----ATACATCCAGCTGGTGGCATTTCTGGGGGAACCGTG 58618
QY 967 LysGlnArgAlaAlaAlaIleProProLleGlnValThrLysValHisGluProProArg 986
Db 58619 AAGCAAGATCAGCCCTC----- 58636
QY 987 GluAspAlaAlaProThrLysProAlaProProAlaProPro-ProProGlnAsnLeuCl 1006
Db 58637 TGACACATGGCCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 58696
QY 1006 nProGluSer-----AspAlaProGlnGlnProGly--- 1016
Db 58697 AGCAGGTAGCATGGGAACGTAGCAGCACACCTCCACTGACCTGCTCCAGCACCCCTCTTG 58756
QY 1017 -----SerSerPro--- 1019
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Db 58817 CTGACTGCCACCTTAACCTCTTTTTCAGCAGAGAAACCGCATTTTTCGGCTTTCCCAAC 58876
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Db	58877	TGAGGGCCCAAGACTAGCACTAGAGCCCAACGCTGCTCATCTCGGCGCTTCCCAT	58936	Qy	1120	gGlnIleGlyAlaIleSer---	1126
Qy	1057	lProProArgGluValIleIysAlaSerProHisAlaProAspProSerAlaPheSerTy	1077	Db	60014	GCAGCTGGGTGGCCATCTCCACAGGTAGTACCTCTGGGGCTGGGTCTCCCATCATCAGGGA	60073
Db	58937	CCCTCCACGGAGGTGATCAAGACTTCCCAACAGCCGCTGACCCCTCTGCTTCTCTTA	58996	Qy	1126	-----	1126
Qy	1077	rAlaProPro-----	1080	Db	60074	GCCTTTTGTAGCCATGGGTGTTTCCAGGATGCTACTGGTGGGAGCCGCTGGGCTCA	60133
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Qy	1080	-----	1080	Db	60134	TCCCTGCGAGTTGGGCAGCTACGGGGCTACGTGGATCTCAGGCTGTGCATTCGCTGC	60193
Db	59057	CTCTTTCAGTGTGCGAGGGTGCATGTGTGCGATCGGATGAGACCTTGGCTGAAGGTGTG	59116	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60194	CTCAGGAGGTGACTCAACGCTCTGGAGGCCCTCAGTTTCATCTCTGTTTCAGTGAGAGGGTG	60253
Db	59117	ACCTGCTCACTCTGTGAAGCTGGGCACCTTCTGAGACTCGGGAAGCTTCCGCACTACC	59176	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60254	GGGAGCTGCAGCTGTACAGGCTATCGAGTGTACAGTCTATAAGCCCTTGGTCACTCTGC	60313
Db	59177	TGCACGCCATAGCAGCCTTGGAGGAACTTGAGCTGGAAAGGGAGGCCAGCGTGGGA	59236	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60314	ATCCTACTGCCCTCAGCACACGGGATCGAAGCAGTCACACTGTGTCTTTACGTGGGC	60373
Db	59237	GGTATTTTCCACCAGTGACTAAGAGGATGTGTCATTAGAGGAGCAGTGGGCAGTCTTGAT	59296	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60374	ACTGGCCTGGGCAGTGTGTCCTCCATTCCTCAGCTGAGTGGGCCGACAGCCC	60433
Db	59297	TGACAGATAGTGTAGAGACTGTTTGGGGGGAAGCCACTAGGTTTTCTATTCTTGATGG	59356	Qy	1126	-----	1126
Qy	1080	-----	1080	Db	60434	CATCTCTGACCTGCATATCCTTAAGTCCAGAGTGGGGCTCTCCCTGTGTCTGAATCTGGT	60493
Db	59357	TCCTTACCACCACTAAAGTAATCCAGCCAGGGGCCAGTGATTAACAGATCAGCAGTGG	59416	Qy	1127	-----GlnGlyMetSerValGlnLeuHisValProTyrSerG	1139
Qy	1080	-----	1080	Db	60494	TGTGATCTGTTTCTTACCCTAGCAGGGGATGTCACTCCAGCTTCGTGTGCTCACTCAG	60553
Db	59417	CTGGCCCGAGGTAGAGCTGACCCATGGGACAAGTGTACTGAGGGAGCTTGGAGAACAGGA	59476	Qy	1139	luHisAlaIysAlaProValGlyProValThrMetGlyLeuProLeuProMetAspProL	1159
Qy	1080	-----	1080	Db	60554	AGATGCCAAGGGCCCCATGGGCCCTCTCACCATGGGGCTGCCCCCTTGGCGTGACCCTA	60613
Db	59477	AAGGCATGCCAGGAGGAAGAACAGCATAGCATGTGCAAAAGGCCAGAACACTCTCGAG	59536	Qy	1159	YsLysLeu-----	1161
Qy	1080	-----	1080	Db	60614	AGAAGCT-GGGTGAGTTCCCAACACCTTGTGTTCTTACAACCTTGGCTAAGGGTGGGC	60672
Db	59537	TCGGGACACTTGAGGCACCGAGCATCTGTACAGCATTAACATTTCCACCAGCAAGCC	59596	Qy	1162	-----Alap	1163
Qy	1080	-----	1080	Db	60673	AGTCCCTGTGGGAGGGCAGCTTGAGACCTCTGTGTATCTCTCACCCGCTCCCTAGCCC	60732
Db	59597	CAGGGATCCCAGTCACTGTCACTGGAAATCCAGGCGGAGGTGACTCTCTGAAAGGCAT	59656	Qy	1163	roPheSerGlyValIysGlnGlnLeuSerProArgGlyGlnAlaGlyProProGluS	1183
Qy	1080	-----	1080	Db	60733	CCTTCAGTGAGTGAAGCAGGAACAGTTGTCCCTCGGGGTGAGGCTGGGGCCACTGAAA	60792
Db	59657	AGGGGGGGATAGCGTCTGACTCTGGGAAAGTCCCTTTTGGCCCTGTGAGGAGAACAG	59716	Qy	1183	erLeuGlyValProThrAlaGlnGluAlaSerValLeuArg-----	1196
Qy	1080	-----	1080	Db	60793	GTCTGGAGTGCCCACTGTCTCAGAGACCTCTGTGCTGAG-AGGTAAGGCTGGGCACAGTC	60851
Db	59717	GATCTAGGGAGGAGTGGAAATCGGGGTGTGGCTTAGAGGCTTGGGTGTGGATCGGGGG	59776	Qy	1196	-----	1196
Qy	1080	-----	1080	Db	60852	ACCTTCACTCTAGAGAGCCTGAAAGCCCACTTACAGAGCTGTTTCTCATCTCTTGAGAC	60911
Db	59777	TGGGGTGGTGACGGTGCAGCTTCAGAGAATCCAGGACTGTGGGTTTCCCGTGGAGTGCT	59836	Qy	1196	-----	1196
Qy	1080	-----	1080	Db	60912	ACCAAGAAGACAGTGGGTGGCTTTACAGATGAGGGTCTTACAGAGTGGGTCTTTTGTGTC	60971
Db	59837	CAAGCCACTGAAGCAGACATGTGGAGAGCCCTCCAAGAGACACTTCTTATTTCTTTC	59896	Qy	1197	-----GlyThrAlaLeuGlySerValProGlyGlySerIleThrLysGlyIleProSerT	1215
Qy	1081	-GlyHisProLeuProLeuGlyLeuHisAspThrAlaArgProValLeuProArgProPr	1100	Db	60972	TTCTAGGACAGCACTGGGCTCGCCACCAAGTGGAGCATCACCAAGGGCTCTCCCAATA	61031
Db	59897	AGGTACCCCTGCTCTGGGCTTCCACATAGTGGCCCGCTCTCTGACAGTCCCCC	59956	Qy	1215	hrArgValProSerAspSerAlaIleThrTyrArgGlySerIleThrHis	1231
Qy	1100	oThrIleSerAsnProProProLeuIleSerSerAlaIleHisProSerValLeuGluAr	1120				

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Qy	1231	-----	1231
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Ds	61266	AGATAGGATAGCCAGCTCATACACAGGCTGTCTAGGAGCCACAGGCGATAGAGTGTCTG	61325
Qy	1231	-----	1231
Ds	61326	GACTGAGAAAGTTACCTGGGCGCAGGAAGAGGAAAGTGTGACATGTTATTATGGCCGGAAG	61385
Qy	1231	-----	1231
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Qy	1231	-----	1231
Ds	61446	CAGTGGTGGTGCAGACTTAGTACCACCGAGCAGGAAGGATGGCGAGTTCACGGCA	61505
Qy	1231	-----	1231
Ds	61506	ACCTGAAGTGTAGCTCAGAGACCTTGTCTTATGAACAGTATGTTATTTCTCGATA	61565
Qy	1231	-----	1231
Ds	61566	GCACTCTGGGAGTCTCGAGAGGACGGTGTGGCAGCAGCATTTGGCACTCGGAAGCCA	61625
Qy	1231	-----	1231
Ds	61626	GGATGAGAGACATTTGACAAATCGGAGGGAGTTACATGTGTGGCTGTGCTGTG	61685
Qy	1231	-----	1231
Ds	61686	CATGCTTGGGGTGGGGAGTGGTGGGTGAGGAGTCACCCACAGATCCGGGTGC	61745
Qy	1232	-----GlyThrProIlaAspValLeuTyrIysGlyThrIleThra	1245
Ds	61746	CTGCCACTCCACCCCTACAGGGCAGCGCCCGCAGACGTCCTCTACAAGGGTACCATCAGCA	61805
Qy	1245	rgIleileGlyLeuAspSerProSerArgLeuAspArgGlyArgGluAspSerLeuProL	1265
Ds	61806	GGATCGTGGTGAGGACAGCCCAAGTCCGCTTGACCGGCGCAGAGAGACACCTTGCCCA	61865
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Ds	61866	AGGGCATGTCTATCATGTATGAGGCAAGAAAGGCCACGTCCTATCTCTATGAAGGTGAGGACA	61925
Qy	1281	-----	1281
Ds	61926	GAGGACAGACAAACCAGGCTCTGGCAGTTAGTGGGTGGCTATGCTCTCTCCT	61985
Qy	1281	-----	1281
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Ds	62046	CCACCTTGTAGGCTGAGGCTTAGCAAGCAAGCACAATAGCAGATAGTACTTCCCTGCCAG	62105
Qy	1281	-----	1281
Ds	62106	CTCGCCCTGCTGGGAGTGTGTGGAAAACCCCTTTGTTGATTAGGAGTCATGAAGACCGGA	62165
Qy	1281	-----	1281
Ds	62166	CTGCAACACAGGCCCCAGACAGCCGTTTGGGCTGTCTCCACTTTGTGAGAGGGCCCC	62225
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Ds	62346	AGGCTCTATAGAGTCTCTTTTAGAACACAGCAGAGCTGAAAGTGATATCAGGCTGCAGGCA	62405
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Qy	1281	-----	1281
Ds	62646	CTGCTTCAGGCTGGGACTGCAGCTTCCCTATTCTTGTAGCCCAAGAGCCCTTAATC	62705
Qy	1281	-----	1281
Ds	62706	CTTGAGGTAAAGTGAACCCCGTGTCTCAGGGAACAGGGCACCCAGCTGCCTCAGGTGC	62765
Qy	1281	-----	1281
Ds	62766	CAGCTGCATGTCTGTGTGACAGCCCCAAAGAGCTAGTAGAGCACTGAGTCACAGCTTGGG	62825
Qy	1281	-----	1281
Ds	62826	AGCCTCCAGAGTCTTAGATTTTAACCTTCCAGCCTGTCTTTGTGGAGATGGGCTGTCTTA	62885
Qy	1281	-----	1281
Ds	62886	TGGCTCTTTTCTGGGGCCAGTGGGTCTGAGGCAGTTCCAGAGTGTCAACCCCGTCAGTCC	62945
Qy	1281	-----	1281
Ds	62946	CAGCCCCAGCTGCCACCTTTCTTTACATAATTTCTTTGTATTTCTCATATAGCCAGC	63005
Qy	1281	-----	1281
Ds	63006	ATGTTCCAAAGTCACCAGTGAACAAGCCACTCTGTCTCTGCGCAGCAGAGGCACACCT	63065
Qy	1281	-----	1281
Ds	63066	GTAACTGGCTCACATGGTCTTGGACTCACACATATCCACTTGTGCAATGCAGAGCT	63125
Qy	1281	-----	1281
Ds	63126	GCAGGCGCTTGTGGAGCTTCCCTGCCGACTCAGACTGTGTGACATCTTTTAGTGTGCAC	63185
Qy	1281	-----	1281
Ds	63186	ATACACCTATGGGTACAGAGCATACCCACCACTTACAAAGCCCGGTGGGATGCCCT	63245
Qy	1281	-----	1281

Qy	1281	-----	1281		AGCCAAAGCTCTTGAAGCGAGAGGACACACACACCCACACCACTCGGACCTGA	64319	Db
Db	63246	GCTCTTTCTGCCAATTGAGCTGGTTTGAGGGTCCCATCTGTGGATGGCAGGGCTCCTT	63305		hrGluAlaTyrLysThrGln-----AlaLeuGlyProLeuLysLeuLysProAlaH	1411	Qy
Qy	1281	-----	1281		CTGAGACCTACAAGCCCGCCCTCGACCCCTCTGGGTCCCTGAAGCTGAAGCCGACTC	64438	Db
Db	63306	CCAGCTCTGCTATTGGCGGGCCTAGCACCGTGCCTGTATGTGCAGGCCCTTGGAGCCGT	63365		isGluGlyLeuValAlaThrValLysGluAlaGlyArgSerIleHisGluIleProArgG	1431	Qy
Qy	1282	-----	1292		ACCAGGGTGTGGTGTAGCAACTGTGAAGGAGCGGGCGCTCTATCCATGAGATCCGAGAG	64498	Db
Db	63366	CCACATCGTGTCTTCTCGGGCTCCAGGTGGTATGTCCGTGTACAGTGTCTTAAGG	63425		luGluLeuArgHisThrProGluLeuProLeuAlaProArgProLeuLysGluGlySerI	1451	Qy
Qy	1292	luApGlyArgSerSerGlyProHisGluThrAlaAlaProLysArgThrTyrA	1312		AGGAGCTGCGCCGACACCTGAGCTACCCCTGGCACCACCGCTCTGAAGAGGGTTCCA	64558	Db
Db	63426	AGGATGAAGAGCAGCTCGGGCCACACCCATGAGACTGCGGCCCTTAACGACACCTATG	63485		leThr-----	1452	Qy
Qy	1312	spMetMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGlu-----	1328		TCAC-CCAGGTACGAGAGTCCAGAGGGGGGCATGGGCAAGCTTGGGGGTGCTAATG	64617	Db
Db	63486	ACATGATGGAGGGCGGTGTAGGCAGGACTGTACCTCAGCCAGCATAGAGGGTAAGTGC	63545		1452	1452	Qy
Qy	1328	-----	1328	-----	CTGCCCTCGTTGCATTGGGTTATAAATGAGGCCAGAGACATCAGCAGCTGGCCCTGGT	64677	Db
Db	63546	CCGCTGTAGCCACTTACCAGGACCGAGCGCTGCCAGGAACCTCCAGGCCACCCAGGCCA	63605	-----	1452	1452	Qy
Qy	1328	-----	1328	-----	CACTGACAGTATTGTGAAACCAAGTCTTATGTCTTAACCTGTCTACTTGACTGCTCCC	64737	Db
Db	63606	GAATGGAAAAGGAGTGGCTCTTGACAAGCTTGGAGGGATCCAGTTAGTTGGGTCA	63665	-----	1452	1452	Qy
Qy	1328	-----	1328	-----	CAGCTCTTACCTGATGATGTATGTCAAGCTAGAGCACTGTCTCTTAATCTTGGTCAATA	64797	Db
Db	63666	ATATTACAGATAGAAACTGAGGCACACCTACTGCAGAATGGGGCCCGAGGAAGTGG	63725	-----	1452	1452	Qy
Qy	1328	-----	1328	-----	GCTTGATGGAAAGAGAAAGACAAACAGCCAGCAAGGGCGCTAGGGGGCTATCCC	64857	Db
Db	63726	GGGGTGTCTTCTGCTGGGTCTTGCATCATGATGGAATAATTGTAGGTAGACACAGCC	63785	-----	1452	1452	Qy
Qy	1329	-----	1335		CTGAGCCAGACCATATGGTGACACCATGCGCTGTCTCCCGAGGACTCATGGCGCGGCCA	63845	Db
Db	63786	CTCCAGACACCATATGGTGACACCATGCGCTGTCTCCCGAGGACTCATGGCGCGGCCA	63845	-----	1452	1452	Qy
Qy	1335	leProProGluArgHisSerProHisLeuLysGluGlnHisIleArgGlySerI	1355		TTAGGTGCCACTCTTCTTTTGGGGCCAGCACCTTAGAAGGCTAAGTCGGGAAGTTTAA	64977	Db
Db	63846	TC---CCTGAGCAGCAGACGCC---CACCTAAGGAGCAGCATCATCCGAGGCTCCA	63899	-----	1452	1452	Qy
Qy	1355	leThrGlnGlyIle-----	1359		ATTGAGGCTAACTAGGCTACAAAGCTGTACTCTAGCTTAATGCCAGTACCACAGTTA	65037	Db
Db	63900	TCACGCAAGGTAC-CTCCCTTATGGTGTGTGGTTCCCGCCCGGGCCCAAGTACAGCTAA	63958	-----	1452	1452	Qy
Qy	1359	-----	1359	-----	TAAAGTTTAATAACACACAGACATTGAGTAGCAATTGAGATCTAGGACCTAGCTGTGCT	65097	Db
Db	63959	GGGGTTGGAACAGAGGGTGAGCTTCCCGCCATGCTATAGGTGGAGTGAATACTTG	64018	-----	1452	1452	Qy
Qy	1359	-----	1359	-----	CCGTGTCGCGGTGGATCCCCCGCCATCTCTCCATGATGTCCAATAATTCCTTCT	65157	Db
Db	64019	GCCCCGACTCAAAGCTTCAGCAAGCAGCGCTTGTCTAGTATTGGGAGGGGTCCAGATT	64078	-----	1452	1452	Qy
Qy	1359	-----	1359	-----	CTGTGGTGCCTCTGAGACCTAACAGGGAATATGTAACTCCAGCTGGGACCGAGCCAC	65217	Db
Db	64079	GAATGGNACTTTAGTCTGTCTGTGGTAAACTGAGCAGTGTGGTTTACTTAGCATC	64138	-----	1452	1452	Qy
Qy	1359	-----	1359	-----	AGCTGGGTGGCAGCAAGTGCATCTGGCTATGGAAATCCATAGCATTTGCAAGATGGTGCA	65277	Db
Db	64139	CTCAGCGCATATGAAGAGACAGGCTTAGAAAAGTCAAGTTCGCATGCCAGGGGCCACAG	64198	-----	1452	1452	Qy
Qy	1359	-----	1359	-----	GTCCCCACTGGGTGAGGAAGGTTGTGTGACCTGAAAGTTAGCCTCACTCTGGAAACCCCTG	65337	Db
Db	64199	GAAGGAAGGATTGTGCTGACCTAGACCGGACCGGCAAGGCAGTGTGACAGCAGTGTCTG	64258	-----	1452	1452	Qy
Qy	1360	-----	1374		GGCGGGTGGGTGACCCCTGGATGTGTAGCCAGACTCAAGTGAGCAGGGCGTCCAGCCTCTG	65397	Db
Db	64259	TGTGCTGACAGGATCCCGAGGTCCTATGTGGAGCGCAGGAGGACTACTTACGGCGGG	64318	-----	1452	1452	Qy
Qy	1374	luAlaLysLeuLeuLysArgGluGlyThrProProProProSerArgAspLeuT	1394	-----			

Db	65398	GACATCATGTCCTGCTAAAGGTCCTGCTCATTGCTCCAAAGGATAGAGATGCCCATC	65457
Qy	1452	-----	1452
Db	65458	CTGTGCAGACATACAGAAAGCGGCATCTGCCAGCCAAATACAGACCTGCACCTCTC	65517
Qy	1453	--GlnGlyThrProLeuLysTyrAspThrGlyAlaSerThrGlySerLysHisA	1472
Db	65518	CCAGGGCACCCACCTCAAGTACGACTCTGGGACCCCTCCACTGGCACCAAGAACAG	65577
Qy	1472	spValArgSerLeuIleGlySerProGlyArgThrPheProProValHisProLeuAspV	1492
Db	65578	ACGTGGCTCATCATCGGACGCCCGCGGCTTTCCTGCTGCCCTGGCACCCGCTGGACA	65637
Qy	1492	alMetAlaAspAlaAArgAlaLeuGluArgAlaCysTyrGluGluSerLeuLysSerArgP	1512
Db	65638	TAATGGCTGATGTCGGGACCTGGAGGCTGCTGCTATGAGAGAGTCTGAAGAGCCGGT	65697
Qy	1512	roGlyThrAlaSerSerSerGlyGlySerIleAlaArgGlyAlaProValIleValProG	1532
Db	65698	CAGGACACGAGTGTGTGACAGGGGCTCCATCACAGTGGGGCTCCAGTGTGTCGCTG	65757
Qy	1532	luLeuGlyLysProArgGlnSerProLeuThrTyrGluAspHisGlyAlaProPheAlaG	1552
Db	65758	AACTGGGCAAGCCACGCAAGCCACTGACTTACGAAGACCAAGGGGACCCCTTCACCA	65817
Qy	1552	lyHisLeuProArgGlySerProValThrMetArgGluProThrProArgLeuGlnGlu	1571
Db	65818	GTCACCTGCCACGTGGCTCCCTGTGACACGAGGAGCCACGCCACGCTTCAGAAAG	65877
Qy	1571	-----	1571
Db	65878	GTCAGTGGTGAGACTCCCTCAGGCTGCCAGCTGGGGAGGAGCAGCTCCTCTAC	65937
Qy	1571	-----	1571
Db	65938	AGGATACCTGGCCACTGCCTCTTGCCACACGACGCTGTCTCTGCTGCTCTACAC	65997
Qy	1571	-----	1571
Db	65998	TGCATACAGGGCCCCCTGATAAGTGTGTTTTTAAATAATTCAGGCTGAGAGAGGCTC	66057
Qy	1571	-----	1571
Db	66058	AGTAGTGCATAAGCATGAAGACACAGAGTTCAATCCCCCAGCACCAATAGCCAGGCA	66117
Qy	1571	-----	1571
Db	66118	CACTCATGCACGTGTAAATCTTATGCTTCACAGTGAGAGCGAAAGCAAGACAGGAGA	66177
Qy	1571	-----	1571
Db	66178	GTCCTCTAAAGTCTGGGCCATAAGTGGAGTTAAATATCCACAGATGTGGAGAGTG	66237
Qy	1571	-----	1571
Db	66238	AAACTGACCTTCAAAATGCTGTGACTTCTCACTACACACCATGGCACATTTCTCCATT	66297
Qy	1571	-----	1571
Db	66298	CATGTGCACACATACACACAGAAATAAAGTAAATCGTTGAAATGAACAGTTAT	66357
Qy	1571	-----	1571
Db	66358	CACCTCGTAGGTTATCTGTCCAGTAGCACTGCTGCTGAAGCCCTGCTGTGAAGCT	66417
Qy	1571	-----	1571
Db	66418	CACCCCGAGTCTGTGTTCCCTCTCTGATTTCTTTTACCTCCCTGACTTCCACTCTCAT	66477
Qy	1571	-----	1571
Db	66478	CTCGATCCTTCTCAGCCTTTCCTGTGTGGGCCCTCTTTAGAGGGCTCCACCTTTGG	66537
Qy	1571	-----	1571
Db	66538	TTCTGTTTTCAGCAACCCCTGTATATACCCCAACACCCTAATTTCAGATGTCCAGGCCAC	66597
Qy	1571	-----	1571
Db	66598	CAGGGAGGCTATGGCCAGTTCAGCCACATCCTGGCTAGGCTTGTAGTGTGCAGAT	66657
Qy	1571	-----	1571
Db	66658	CTGTGTTTTCATTCATTGTCTCAGGGGCGCACTTCCCAAACCATTGAGATCATTTCTCTCT	66717
Qy	1571	-----	1571
Db	66718	CAAGCCTGTGTCTTCTACTTTTGTGTTTCATCTCCGACCTGGAGCAATGGCTCTTGG	66777
Qy	1571	-----	1571
Db	66778	GGCTCAGGGTTCTTGGCTGTCTTTTCTTGGGGTGTCTCCAGCCCATGATAAAGTCAGACT	66837
Qy	1571	-----	1571
Db	66838	GGTGAGTGAATGCGGAATGTGTACAGGAGTAAATGATATTTTCCAGGGGACCAAC	66897
Qy	1571	-----	1571
Db	66898	AGCAGAGGGCAAGAGGCCCTGGGGTGTGTGACAGCTCAGCCTGTGTGGCCCCACTGAGGC	66957
Qy	1572	-----GlySerLeuSerSerSerLysAlaSerGlnAspA	1583
Db	66958	TGAGGCTACTGTGACCTGTCCCAACAGGCAGCTCTTATCCAGCAAGGGCTCCAGGACC	67017
Qy	1583	rgLysLeuThrSerThrProArgGluIleAlaLysSerProHisSerThrValProGluH	1603
Db	67018	GGAGCTGACATCTACACCCCGGAGATCGCAAGTCCCAAGTCCCAACAGCACTGTGCCGAGC	67077
Qy	1603	isHisProHisProLysProTyrGluHisLeuArgGlyValSerGlyValAspL	1623
Db	67078	ACCACCTCACCCCATCTCCCTATGAGCACTTCTCCGGGGCTGACTGGTGGGACC	67137
Qy	1623	euTyrArgSerHisIleProLeuAlaPheAspProThrSerIleProArgGlyIleProL	1643
Db	67138	TGTACCGTGTGCATCCCATTTGGCCTTTGACCCCACTCCATACCCAGGGAGTCCCTC	67197
Qy	1643	euAsp-----	1644
Db	67198	TGGAAGCAGGTGGGTGTCTGGGCCCTGTAGATTTGGGGCTTAATGATTCCTCTCTGG	67257
Qy	1644	-----	1644
Db	67258	GTGGGCTCTTGGGGTCTGGAGAGTTGGGGCTAGGCTTAGTATAGAGATCATCCCTGGTT	67317
Qy	1644	-----	1644
Db	67318	AGCCAGGGCAGGTTCCAGGGTGGGCTTGGGATCCTGTCTCTCAGTGGGCTTTCTTTCC	67377
Qy	1644	-----	1644
Db	67378	TGGAGGATTCATCTGTACCTTGCAGTAAGTGGGGGCTCAAGTGAGTGCCATGACTTGAG	67437
Qy	1644	-----	1644
Db	67438	CTTTTAAAGGCTCTTTTGTAGGGTGTCCAGGAGCTATATATTTTGACGATATATCTGT	67497
Qy	1644	-----	1644
Db	67498	GAGCACTTCCAAAGCATTCACAGACACACCCCAATGATGAGGGAGCGAGTCTTAAGC	67557
Qy	1644	-----	1644
Db	67558	TCTGTGTGTACTGGGGAGGCATGTGGGTGCACAGGAGGAAGCTGAAGTGGGAGT	67617

Qy	1645	-----AlaIalaAalAt	1649
Db	67618	ATGAAGATAAGACATGGCCACCTGACCTTCCTCCTCCCGCCAGCGAGCCT	67677
Qy	1649	yRtyrLeuProArqHisLeuAlaProAsnProThrTyrrProHisLeuTyrrProProTyrrL	1669
Db	67678	ACTACCTGCCCGGCATTGGCCCCAGCCCCACCCTTACCACACCTGTACCCACCTTACC	67737
Qy	1669	eulleArqGlyTyrrProAspThrAlaAlaLeuGluAsnArgGlnThrIlelleAsnAspt	1689
Db	67738	TCATCCCGGCTACCTTGACAACCGCGGCTCGAGAACCGCCAGACCATCAATGACT	67797
Qy	1689	yrileThrSerGlnMeHiHisenThralaThrAlaMetAlaGlnArgAlaAspm	1709
Db	67798	ACATCACTCGCAGCAGATGCACCAACCTGCTCCGCGCATGGCCAGCGTGTGACA	67857
Qy	1709	etLeuArqGlyLeuSerProArgGluSerSerLeuAlaLeuAsnTyrrAlaAlaGlyProCa	1729
Db	67858	TGCTGAGGGGTGTCTACCCGAGAGTCTCGCTGGCCCTCAATTAATGCGCTGGGCCAA	67917
Qy	1729	rgGlylle-----	1731
Db	67918	GAGGTGA-GTTACCCAGGACTGCCCCCATCAGCAGAGGCTTGCAAAAGCAGGTGCTTT	67976
Qy	1731	-----	1731
Db	67977	GTGTGCACCTGTGAAGGTGGAGAGGGGTACAGTTGCCAGGTGAATAGGTGTGCA	68036
Qy	1731	-----	1731
Db	68037	TGCTGGCTCCTGGGAGAAGCAGGGTGGTCTGCTTAGATCTTTTTCACGTCTAGCAGTG	68096
Qy	1731	-----	1731
Db	68097	TGTAAGTAGCAGGCACCTCTGTACCATGCTGTTGTTCTGAGACTTTGGTATGAGCCA	68156
Qy	1731	-----	1731
Db	68157	TCITTTTGACATTCAAGAGATCAGAAACAGGCTGGACCGGGTGTGTGATACCTTTTCTCT	68216
Qy	1731	-----	1731
Db	68217	AAGTATCGGGAGGTTCAAAGCCAGCCTCAGCTACATAAAGCTTGAGGTGCCAGCTGGG	68276
Qy	1731	-----	1731
Db	68277	CTATGTGAGTCCATTTTAAATACAAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	68336
Qy	1731	-----	1731
Db	68337	AAGAAAGGAATGAGTGTGAAGCCTTTTGGAGCACTGACTTCCAGAGCCTGTGAAGAGCCC	68396
Qy	1731	-----	1731
Db	68397	AGGTCACTTTGTACAGACTGTTGAGCAGCTCTGTGGGTTTTCAGAGGGTGATGCGAGTT	68456
Qy	1731	-----	1731
Db	68457	TCGGTTCAAAGATGTTGGTTGAGAGACACTACCGGTACAGGCTTTCAGNAGGAGCGCTG	68516
Qy	1731	-----	1731
Db	68517	GGGCCAAGCCTGGCCCTAGGAGGGGTACAGCAGGTGCAAGGTCTCAGGCTTACACCTT	68576
Qy	1732	-----Ilea	1733
Db	68577	GGGAACAGGAGGTTCAGAACCTGCAGCTAATACCCCCCTGACCCCCCTGACGGCATTTATCG	68636
Qy	1733	spleuSerGlnValProHisLeuProValLeuValProProThrProGlyThrProAlat	1753
Db	68637	ACCTGTCCCAAGTGCCACACTGCGCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	68696
Qy	1753	hrAlaMetAspArgLeuAlaTyrrLeuProThrAlaProGlnProPheSerSerArgHis	1773

Db	69745	GATGAAGCGGTAGATAGACATATGGGGCAGATGTTTGGATGGATGGGTGGATGGATGGAT	69804
Qy	1898	-----	1898
Db	69805	GAGTTGGAGCAGATAGATAGTGTAAAGTGGATATGTGCTGGTGGATGGATGGT	69864
Qy	1898	-----	1898
Db	69865	GAATTGGATAGTGGATATGTGGACTGATGGACAGGTAAAGCAGACACACAGATGAATGGG	69924
Qy	1898	-----	1898
Db	69925	TATACACTGGGCAGCTGGATGGTTGTATCACTGTGTAGATGATGATAGATGAAGTGGATG	69984
Qy	1898	-----	1898
Db	69985	TATAGAAAGGAAGATAGGGGTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT	70044
Qy	1898	-----	1898
Db	70045	TGGGTCCACGGATGGCTGGATGGACAGCAGATGAGTGGATAGCAGAGTGGGTGAATGAA	70104
Qy	1898	-----	1898
Db	70105	TGGATGGAATACAGGTGGATGATGGGGTGGTGCATGGAGTCCGTTGGTAGTCATTA	70164
Qy	1898	-----	1898
Db	70165	GTGTATAAGGCCAGAAATACAACTTCAGAGAACAAGACTGGGAGCTTAATGTGAGGCC	70224
Qy	1898	-----	1898
Db	70225	GCAGGGCTGGTGTGCTCAAGGCGCTGGTGGCGGGATGCGCTGCTGCTGAAGTCAG	70284
Qy	1898	-----	1898
Db	70285	TCTCATGCTTCTGGCTCTCATGCCACCACTGCTGAGAGGCTCCGCACTCCTGCGGACT	70344
Qy	1898	-----	1898
Db	70345	TCTAGGCGTGCCTCTACTGCGCCTGCTGAGCCTCTGCGCCTCCCGCACCGAGTCTCT	70404
Qy	1898	-----	1898
Db	70405	TCTCTGACCTTGGGAGAGATAGTCTGCTCTGTCACTGTCTTCCAGAGCTCGGG	70464
Qy	1898	-----	1898
Db	70465	CACCCCTTGCTTAAGTGTGTATTCTGTATCATCTAGGAGGGTAAGAAGCTTTAGGTGATA	70524
Qy	1898	-----	1898
Db	70525	GGGACTGAATAGACCGAGCAGCATAGGAGGTGACTCAGGAGGGCACTTGTCTTGGG	70584
Qy	1898	-----	1898
Db	70585	AGCCTCAGAGATGAGATCTAGGAGGGGACTCTCAGTCAGGACTCTGAAGGTGTGAGG	70644
Qy	1899	-----ArgSerThrSerTh	1903
Db	70645	TAGGAAGCCATTGGCCAGCACTGCCCTGACTCTCTCCCTGTCTGTGCAAGTCCACCTCCAC	70704
Qy	1903	rSerSerProValArgProAlaAlaThrPheProAlaThrHisCysProLeuGlyI	1923
Db	70705	CTCTTCCCTGTCCGCCAGCTGCCACATTCCCACTGCCACCTGGCCTTGGTGG	70764
Qy	1923	yThrLeuAspGlyValTyrProThrLeuMetGluProValLeuLeuProLysGluAlaPr	1943
Db	70765	CACCCCTTGAAGGGTCTACCTTACCCTCATGGAGCCGCTCTGTGTACCAAGGAGACCTC	70824
Qy	1943	oArgValAlaArgProGluArgProArgAlaAspThrGlyHisAlaPheLeuAlaIysPr	1963
Db	70825	TCGGGTGCGCCCGCGAGCGGCCCTGTGTGACGCTGGCCATGCTTCTCTCACCACCAACC	70884
Qy	1963	oProAlaArgSerGlyLeuGluProAlaSerSerProSerLysGlySerGluProArgPr	1983
Db	70885	CCGGGCCCGG-----GAGCCCGCTCTCACCAGCAAGAGCTCCGAGCCCGATC	70935
Qy	1983	oLeuValProProValSerGlyHisAlaThrLeuAlaArgThrProAlaIysAsnLeuAl	2003
Db	70936	CCTAGCACCCCGCAGCTCCAGCCACAGCATCGCCCGCACCCAGCAAGAGCCTTGC	70995
Qy	2003	aProHisHisAlaSerProAspProProAlaProProAlaSerAlaSerAspProHisAr	2023
Db	70996	ACCCACCATGCCAGTCCGACCGCGCGG-----CCACCTCGGCTCAGATCTGACCG	71052
Qy	2023	gGluLysThrGlnSerLysProPheSerIleGlnGluLeuGluLeuArgSerLeu-----	2041
Db	71053	AGAAAGACTCAAAAGTAAACCTTTTCATCCAGGAATGGAACTCGTCTCTCTGGGTAA	71112
Qy	2041	-----	2041
Db	71113	GACCACCTGTAGACGGGCCAGTTTCATAGAGCAATAATCACGCGTCAAAATTCGTACGA	71172
Qy	2041	-----	2041
Db	71173	AAGGGGGCGGAGAGAGGTTTCGTGGCCACAGACTCCCTCGCGCAGCGTAAGACATC	71232
Qy	2041	-----	2041
Db	71233	CGGCCCGCGCTGCCACCCCATCTGTGGCTAAAGATAATTTTCAGATCTTTGCTTTTA	71292
Qy	2041	-----	2041
Db	71293	ATTTTTCCTTTTTCGTTGGTTTGGTATTTTGTTCGAGCTCGTCATCTCTGGTCAG	71352
Qy	2041	-----	2041
Db	71353	TTGGCAGCTGTGGTGACTCCGCCACACAGGGCCCTCATCGTTTGCCCATCTGTCTCT	71412
Qy	2041	-----	2041
Db	71413	ATGAGTTTTTTTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT	71472
Qy	2041	-----	2041
Db	71473	CTTTTGGATTTTTCACCTTTTTCCTTTTAATGAATGGATCTGTGGTTGGACTCCGACC	71532
Qy	2041	-----	2041
Db	71533	GGCCTCCCATCTCCCGCACCACTGCACTTCTGTTTGGGGAGTGGGGATGCAAGGGG	71592
Qy	2041	-----	2041
Db	71593	TACCACTGACTGTGCTACTGTTCTGTGAGGAAGTCAAGGCAGGAGCGAGGGGGGAG	71652
Qy	2041	-----	2041
Db	71653	ACAGGTGGGGGGGCTGGGTGCCACCTCTCTTCCACACACAGCATAAAGCCCAA	71712
Qy	2041	-----	2041
Db	71713	GGGAGTGATCAGGGCAGTGGGCTGGGCAAGGCAGGCGCTAGGGACACAGTTGTCTAG	71772
Qy	2041	-----	2041
Db	71773	GGACAGGTGTCACTCAGCTTGAACCCACACCATCACACCTTGACCCCATGCACACTCA	71832
Qy	2041	-----	2041
Db	71833	AGCCCTCTCCAGTTTCTCCACCAACCACTCCCCAGTCTCTCTCTTCTACCCAAAGCC	71892
Qy	2041	-----	2041
Db	71893	CACACTGCCCCAAGCCAGACTCCCAACAGTCCCTTTGGGTGTGTCTGTATCTCTGATACATGGA	71952

Qy	2041	-----	2041
Db	71953	ACTGTCTGTCACTTGCATTCTCTCTTCTGGCCCACTAGGCTTAGATAATTTCTCTTC	72012
Qy	2041	-----	2041
Db	72013	ATCTTGAGGCCCACTGTGTGAGGAATGGCTATCCCAAGCACCCCCCAACCAAGCCC	72072
Qy	2042	-----GlyTyrHis--GlySerSerTyrSerP	2050
Db	72073	ACCCACCTCTGACCCAGCTCACCTGTTTCAGGTTACCAAGTGAGCTGGCTACAGCC	72132
Qy	2050	roGluGlyValGluProValSerProValSerProSerLeuThrHisAspLysGlyL	2070
Db	72133	CCGATGGGGTGGAGCCCATCAGCCCGGTGAGCTCCCGCAGCTCAGCCACGACAAAGGGC	72192
Qy	2070	euProLysHisLeuGluGluLeuAspLysSerHisLeuGluGlyGluLeuArgProLysG	2090
Db	72193	TCTCCAAACCTCTGGAAGAGCTAGAGAAGAGCCACTTGGAAAGGGAGCTGCGGCACAAGC	72252
Qy	2090	lnPro-----	2091
Db	72253	AGCCAGGTAACCCGGGAGAGTGGCAGGTGGGAGACTAAGGCACCGCTCCACGCTGTC	72312
Qy	2092	-----GlyProValLysLeuGlyGlyGluAla	2100
Db	72313	CCGAGGCCCTGACAAGCTCTGCTCGCTCTCTTAGGCCCCCATGAAGCTCAGCGCGAGGCT	72372
Qy	2101	AlaHisLeuProHisLeuArgProLeuProGluSerGlnProSerSerSerProLeuLeu	2120
Db	72373	GCCCATCTCCACATCTGCGGCCACTGCGGAGAGCCAGCCCTCATCCAGGCCACTCTCTC	72432
Qy	2121	GlnThrAlaProGlyValLysGlyHisGlnArgValThrLeuAlaGlnHisIleSer	2140
Db	72433	CAGACTGCCCCAGGCATCAAAAGTACACAGAGGGTGTGTCACCTGGTTCAGCATCAG-	72491
Qy	2140	-----	2140
Db	72492	CGTAAGTGTCTATTTCTGGGCCCCCACCATTTGGGGTGGATAGGAGTGAGTCCCATAG	72551
Qy	2140	-----	2140
Db	72552	TCAGACAGATGTAGCATGCATGGCCACTACACTCAGTCTGTGGCGGTGTCAACATA	72611
Qy	2140	-----	2140
Db	72612	AGGTCTGCTGGGACACTCACCCAGGAGACCAAGAGTCAGATCAGGGTTCGCGCTACT	72671
Qy	2141	-----GluValIleThrGlnAspTyrThr	2148
Db	72672	CTACACTGAAAGTCCTGACCTGCCTCTCCACAGAGGGTCAATTACGAGGACTACACG	72731
Qy	2149	ArgHisHisProGlnGlnLeuSerAlaProLeuProAlaProLeuTyrSerPheProGly	2168
Db	72732	CGCCACACCCCGCAGCAGCTCAGTGGGCCCTCTCCGCCCTCTCTACTCTTTCGCCGA	72791
Qy	2169	AlaSerCysProValLeuAspLeuArgProProSerAspLeuTyrLeuProProPro	2188
Db	72792	GCCAGCTGCGCTGTCCTGGATCTTCGGCGCCACCCAGTGACCTTACTCTCCACCCCCC	72851
Qy	2189	AspHisGlyAlaProAlaArgGlySerProHisSerGluGlyGlyLys-----	2204
Db	72852	GACCATGGCAACCCAGCCCGGGATCCCCCAGTGAAGGGGGCAAAAGTGAGGATAT	72911
Qy	2204	-----	2204
Db	72912	ACTCATATCTGTGTGATGCTTGGCTGAAGGATATTGGGGTAGGATGAGCTTGACTGTG	72971
Qy	2204	-----	2204
Db	72972	TTGGGCTAAATGGGAACCTGAGGCTCAGGGATACAGAAGTTCACTAAGGCTCCAGAACCA	73031
Qy	2204	-----	2204
Db	73032	CACAAAGTCTAATCACGAAGGTGGCACACCAAGGCTCCCATGTGCCAACTAGTGTCTCT	73091
Qy	2204	-----	2204
Db	73092	ATATATCCCAACTCAGCTAGGGGTCTGATGTCCCATGCCCATTTAGCAGATAGGAAAACT	73151
Qy	2204	-----	2204
Db	73152	GAGSCATAGAGAAGTGAATTACCATCCATACCATGACACACATACTTACCCCTGGCTGGC	73211
Qy	2204	-----	2204
Db	73212	CTGAGGCTCGGGCATGAGAGAAGCTGGGCCCTTACCTAGGCTTTAGGAGCGAGTGAGGC	73271
Qy	2204	-----	2204
Db	73272	ATCTTGATGAGTTTGAATTTTAGAAGCACCGGTAACAGACAGTGAAGTTCTGGCATGGGTG	73331
Qy	2204	-----	2204
Db	73332	CCTCAGTGTGTGGSCACACACTCTACTCAGGTGAGATAGCTCTGCCAGGCTGAGGCAGG	73391
Qy	2204	-----	2204
Db	73392	AGGATTTGTGAACCTTCAGGGCAGTCTGGGATGTACTGCAAGAACCCGACTCAAAAATCAAC	73451
Qy	2204	-----	2204
Db	73452	AAAGCTTACAAGTCTTTTAGTATTCTCAGAAGATCGTAGGCCACTGGGGTCTCCAT	73511
Qy	2204	-----	2204
Db	73512	ACCTCAGCTGCAGAGTGGCCATTTACAGGGAATGTGCAGGGCCCCCGCTGGACAGTGG	73571
Qy	2205	-----ArgSer	2206
Db	73572	GGTCTCTCATATCGGGTAGAACTTCACCTCAGCTAGGACGCTATCTCATCAGGTCC	73631
Qy	2207	ProGluProAsnLysThrSerValLeuGlyGlyGluAspGlyIleGluProValSer	2226
Db	73632	CCAGAACCCAGCAAAACATCGTCTCTGGGACAGTGCAGGATGCCATTGAGCTGTGTGCC	73691
Qy	2227	ProProGluGlyMetThrGluProGlyHisSerArgSerAlaValTyrProLeuLeuTyr	2246
Db	73692	CCACCAGAGGCATGACTGAGCCAGGACATGCTCGGAGCGCTGTGTACCCACTCTGTAT	73751
Qy	2247	ArgAspGlyGluGlnThrGlu-----	2253
Db	73752	CGAGACGGGAAACAGGGCGAGCCAGGTAGCCACAGCAAAATCCGGCTTTAGAGATGGT	73811
Qy	2253	-----	2253
Db	73812	GGTGTAGTTCATGTATACCCCAAGGCTCGGCCCTCCCATATGAGAGCCCATTAATCCCT	73871
Qy	2253	-----	2253
Db	73872	CACAGCTCAGCGGGCTGATAGACCTTCAGGGGCCCTTCAGTTGCAGACCCCTGTCTGGC	73931
Qy	2253	-----	2253
Db	73932	ATCTGTGTGCTGGCATCCCTGTCTGTGGATCTCAGCCTGAGCCATGCCCTGTTTATC	73991
Qy	2253	-----	2253
Db	73992	ACTTGTGGTGTATCTGGGAATGAACTAAGTTGAACAGACTGGGTGGGGTGGACATGGA	74051
Qy	2253	-----	2253
Db	74052	CTTCAGGGAGGGTGTGACCTGCACCTGTCCAGTTCCCTGGGATTTCTTGTGTGATCTA	74111
Qy	2253	-----	2253

Db	74112	GCAATAAGGATTGCTGGGGCAATTTCACAGCGTACCTGGGATGGGAACCAAGCTGTGCTCT	74171	QY	2322	-----	2322
QY	2253	-----	2253	Db	75251	GTTTGTGGGGCTTGGGGCTGGGGCACGTCACCAAGTGTGACCTGAGGATTGGCCTTGG	75310
Db	74172	TAGCACTCACGGTAGCTCAAGTGTGAGTCCCTGTGCTAAAGGTCAAAATGCCACG	74231	QY	2322	-----	2322
QY	2254	-----	2265	Db	75311	GGTACAGAGATTCCAGGTGCGCGAGGCATCTTTACACTAAAGTCTCTGGCCATTTTCTA	75370
Db	74232	CTGCTGACCCGTGTGCTCTGCTGCTCCGCG-AGGATGGGCTCTAAGTCTCCAGGCAACAC	74290	QY	2322	-----	2322
QY	2266	SerGlnProAlaPheSerLysLeuThrGluSerAsnSerAlaMetValLysSer	2285	Db	75371	AATCAGATGCAGCGCAGTAAATGTAGGGGAAAAGTGTCAAACTCACGTGCGAGTTTGTGGCAG	75430
Db	74291	AGCCAGCCGCGAGCCTTCTTCAGTAAGTGTGACTGAGAGCAACTCCGCCATGTGTAAGTCG	74350	QY	2322	-----	2322
QY	2286	LysGlnGluLeuLeuLysLysLeuAsnThrHisAsnArgAsnGluProGluTyr	2304	Db	75431	AAGTCTCAGGCTTTTCAGTATGTGTGCTTGGGGCTTAGAGCATCCGCTTCCGCTTATTA	75490
Db	74351	AAGAAGCAGGAGATCAACAGAAACTCAACACCACCAACCGGAACGAGCCAGAAATACAGT	74410	QY	2322	-----	2322
QY	2304	-----	2304	Db	75491	TCACGTTGCCCTCGGAAAGAAAGCTTGTCTGTGGGAACAAATGGGCTCGGTGACTGTGTGTC	75550
Db	74411	AAGGGAAAGCCAGGGCTAGAGCAGGACCGGGAGGAGATAGTACTTTAAACCTTACCA	74470	QY	2322	-----	2322
QY	2304	-----	2304	Db	75551	ACAGGGGAAGCTGTGAGGACTTAAATCCAGGCCAGAGGAACAGGCAAGGTCCCTACTTCC	75610
Db	74471	TGGAAGAGCCCAAGTTCTGCCAGTTGGTACTAATCTGACAAACAGCATATAGCACTTTGGT	74530	QY	2322	-----	2322
QY	2304	-----	2304	Db	75611	TTATTTGTGTGAGCCTTGGGCTTAGGGAATAAGGTGGCCAGATTAAACCTTGGGGACAT	75670
Db	74531	AATGCCCTGCACACAGTAGGTAGTCACAGGAAAGCTGTAGAGACAGCCCTGTGTGGGTGC	74590	QY	2322	-----	2322
QY	2304	-----	2304	Db	75671	TTCCAGAGACCAACAGGACCTGTAAAGGGATGGGGTAGGATCTCGGACGGACAGCCGTG	75730
Db	74591	TGAGGACACAGCACACTACTCCAGTTTCATGTGCAGACCCGGTGCTTTCACACGGC	74650	QY	2322	-----	2322
QY	2304	-----	2304	Db	75731	GGGCTTTCTGAGCCTCAAGCAGAGGAAACTGACCGAGACAGGAATGTGTTGGAGAT	75790
Db	74651	TGATGTGGTGGACAAGGACTCATGTCTTAGCGCAGGGTCACATGGGCCATATGCTTAC	74710	QY	2322	-----	2322
QY	2304	-----	2304	Db	75791	GGGTGTTCTAGAGTGTGCTAAATCTTGACATAGGTTCTAGACACCTGGGTGTATATGCA	75850
Db	74711	AAGAATGCACCGGAAGCAACATGACAGCTTTGCACTGTCCCTCCCGAGGTGSCCT	74770	QY	2322	-----	2322
QY	2304	-----	2304	Db	75851	TATAGATAGGTAATACAGTGAATTTGTGCTAAAACTAACTTAGTTGTCTCTCACACA	75910
Db	74771	GGACAGACAGCAAGGTTCTTCTTTCTGGAGTATAGAGCCCTCACAGGTAAACAGAGGC	74830	QY	2322	-----	2322
QY	2304	-----	2304	Db	75911	CACACACAGCATCCTCAACATCGCCCTTAAATGTTAGTTCTCAAGACATGTTTCCA	75970
Db	74831	CTAAGTAGTGACCAACCGCTGAGTAAACCTGGAGCATCAGGTGCTGTTGTGCCAG	74890	QY	2322	-----	2322
QY	2304	-----	2304	Db	75971	GGCTAGCCAGTGACGTTCAACACCAACAAAGGTAGATGAGAGAAAAGTTATGCTGT	76030
Db	74891	ACATTCAACTCAGACTGTACGGGGGCAACAGAGGGGTGCAGATCTCTAGGACCTGTGAG	74950	QY	2322	-----	2322
QY	2305	-----	2313	Db	76031	GCCAGTGCCATCAGGTCAACAGTCAACACACGAGACAGGCCAGGACCGGTGCTC	76090
Db	74951	CTCAGCCTTCCCACTTGTACCTGCTCTAGATATTGGCCAGCCTGGACGGAATC	75010	QY	2322	-----	2322
QY	2314	PheAsnMetProAlaIleThrGlyThr	2322	Db	76091	CATCAGGAACTCCCTCTGTCCCTTTTCTGTGTACTCTCTCTCTCTCTCTCTCTCTTAT	76150
Db	75011	TTCAACATGCCCGGCATCACTGGAGCAGGTAAACCTCCTGTGTGTCGCGATGGCAAACTC	75070	QY	2322	-----	2322
QY	2322	-----	2322	Db	76151	TCTGGATGTAGAGAGTGTGGGTGGGGCTTGTATTTAAGGTTGAATTTGTGTGTG	76210
Db	75071	CCTTCCCACTGCTGACTTGGGGACAAGGAGCCTTAGCCTCTCCCTGCTCAGTGGACC	75130	QY	2322	-----	2322
QY	2322	-----	2322	Db	76211	TGTGCGGCGCGTGTGTGCGTGTGCGCGCGTGTGTGTGCGCATGCAATTCACCCCTGTT	76270
Db	75131	CAGATGACACAGATGGCAGCCTCCACTGCTAGGGTCTCTCCCTACATGAGGAGTGCCC	75190	QY	2322	-----	2322
QY	2322	-----	2322	Db	76271	GGAAAGTTCAGCTTTTCTTGGTAAACCTTTGCTTAGCACTGTGGGCACATGACCAACATGA	76330
Db	75191	AAGGTTTGAAGGTACAGGGTCCCTCAAGTGGGTGTAGGTACACCCCGGAAACACTTGGCCA	75250				

Qy	2322	-----	2322
Db	76331	CCAGCCCTGGCCGAGCTTGCCCTGAACCCAAAGCCGAGGCTGCCAGAGTCACCCAGTGA	76390
Qy	2322	-----	2322
Db	76391	CTGTCCCTTCATCCTCAGAAAGCCTGGCTAGTTTACAAACAGAGGCTTGCCAGCCAGCA	76450
Qy	2322	-----	2322
Db	76451	TGTTTGGCCATGTGGCTTTCACAAGGCTCAGGACGCTGGAGGTTTCACAGGCAATCAGAG	76510
Qy	2322	-----	2322
Db	76511	ACTGGCAGTGGCATGGGCTAGGAATCCTGTGATGACGTGCTCATTTGTGTGTTTG	76570
Qy	2322	-----	2322
Db	76571	TTGGTGTGTGATTTGGGTTTTTTGGTTTTTTTGGTTTTTTTGTTCATTTGTTTGGTGA	76630
Qy	2322	-----	2322
Db	76631	GGGTGGTTGGCTCGATTGAGCTTGCCACTGTTTGTGTTCTTTTCCATCTGGATTGGAG	76690
Qy	2322	-----	2322
Db	76691	CAGTTTGTGATACTTGGGATTGAAGCACTCAACCCAGCAAGTGTCCCGTCTGTAGTGA	76750
Qy	2322	-----	2322
Db	76751	GCAACAACACAGCCCTTCTCTGAGGGCAGGTCTCTCGGACAGGTCTCTCGGACGCCAGGCTAGCATGGA	76810
Qy	2322	-----	2322
Db	76811	CTGCACTGAACCTCCCTCTGTAGACTAAGCTAGCTCAGAAATAGCTGGGTTCCAGGCCT	76870
Qy	2322	-----	2322
Db	76871	ACTAATCAGGCTCCAAACCTCAGGAGGCTCGGAAGCATCCAGTGAGAAGGGGATGCCTG	76930
Qy	2322	-----	2322
Db	76931	CCTGCCCCAGCAATTAACAGAGTCCAGAGACAAATTCGGGGGGGGGGGGGGTACT	76990
Qy	2322	-----	2322
Db	76991	AGGAGGTTAAGCAATTAAGAACCATCACGAATAATAGTTTGGAAAAAATTAAGTTA	77050
Qy	2322	-----	2322
Db	77051	CAGAAAGCCATCCTCAGACTGTGGCTCTCTAGGCGAGGTCGGGATGAGTGTGAGCAG	77110
Qy	2322	-----	2322
Db	77111	GCTGGAGCCCAAGCAGTCTGGGATTCATATACCGATGGAATAATGGTGTGTAGCGTGGCA	77170
Qy	2322	-----	2322
Db	77171	GTATTATGTGAAGAGAGATTCTCTGACAGGGAGATTTTTCATCTGGCAGATAGACC	77230
Qy	2322	-----	2322
Db	77231	CAGGAATTATGAACCCCGAATTCATAGATAAACACAACTTGGAAACCCAGAAATCATTG	77290
Qy	2322	-----	2322
Db	77291	TTCTTTCTGTGCAATGTTAGCTTCTTTTGTATCCACAGAAAGGGGTGTGTGTGTGT	77350
Qy	2322	-----	2322
Db	77351	GTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	77410
Qy	2322	-----	2322

Db	77411	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	77470
Qy	2322	-----	2322
Db	77471	TGCAGAGGCTCAGTGGAGTCTGCAACATCTTTAAAGGCCACTTTTGTGATTGACCACT	77530
Qy	2322	-----	2322
Db	77531	CTGTCTTGTTCATGGGGCCGGCCAGCCAGGGCTGGAGTGACCCCTTACCTGTCTCAGTGC	77590
Qy	2322	-----	2322
Db	77591	TGTCCTGCTTGCACGCACACAACATGTCATGGCTGTGACCCCCACCCACCCACCCCTT	77650
Qy	2322	-----	2322
Db	77651	GTGCCAGCTCTACCTTTCTCTGGCTCCTGTGGGGGAGACATGGGGGAGGGAGGCAA	77710
Qy	2322	-----	2322
Db	77711	GCCTAGTTACAGGGGATCAGGCGAGGTCCCTAAACCCCTTGTAGAAAAGGGACAG	77770
Qy	2322	-----	2322
Db	77771	CAGGGGGTCTTATCTTTTGGTCCACTTCTCTCCATCATCCTTCTCTAGAAATCTACCCAC	77830
Qy	2322	-----	2322
Db	77831	CAGTAAGACCCAGCTGGACTTCTGTCCCTGTCCCAGCACCTAGCTCCAGCTTGACTCA	77890
Qy	2322	-----	2322
Db	77891	ATACCACAGCTTCTTCCCTTGGCCGCCCTTGGGCCATCCACGTGGAGTCAAAATTTTA	77950
Qy	2322	-----	2322
Db	77951	AAATAGCTCAGCTGGGATTGGAGTATAGAAATAGAGCTGGGGACCCCTTTAGCC	78010
Qy	2322	-----	2322
Db	78011	ACCCAGAGCCCTTCCCTGGAAACAGCCATGAGCTGAGGAGACAGTCAAGAACCTCATCAG	78070
Qy	2322	-----	2322
Db	78071	CACCAACAGAAAGCGGGCTGGAGGATGAACGATGCTCGGCAGATGTGTCTCACTGT	78130
Qy	2322	-----	2322
Db	78131	GTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTA	78190
Qy	2322	-----	2322
Db	78191	TCCTCGCAACCTCTGGCTCCCGGGCCCCCGCCCCCTGTGTGTGTGTGTCTCTCTCTC	78250
Qy	2323	---GlyLeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMetGly	2341
Db	78251	CCAGGCTTATGACCTGTAGAACCCAGGCGGTGCAGAAACACGCCAGCACCAACATGGGG	78310
Qy	2342	LeuGluAlaIleIleArgLysAlaLeuMetGlyLysTyrAspGlnTrpGluGluSerPro	2361
Db	78311	CTAGAGGCCATTATTAGAAAGGCATCATGGTAAATATGATCAGTGGGAAGAGCCGCCG	78370
Qy	2362	ProLeuSerAlaAsnAlaPheAsnProLeuAsnAlaSerAlaSerLeuPro---AlaAla	2380
Db	78371	CCCTCGGCGCCAAATGCTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT	78430
Qy	2381	MetProIleThrAlaAlaAspGlyArgSerAspHisThrLeuThrSerPro-----	2397
Db	78431	ATGCCATAACCACTGCTGACGAGGAGTGACCAACGCACTCACCTCGCCAGGTCTGCAG	78490
Qy	2397	-----	2397

Db 78491 GCCTGCCCTGCGCGCGCGCGCGCGCGCTGTGTCTCTCTTATCCCGGTGTCT 78550
QY 2397 ----- 2397
Db 78551 TAATCCTCTACCTTCCCGCCCTCAAGCTTGGAGCCTGTGACCTTATTTTGTGGTTT 78610
QY 2397 ----- 2397
Db 78611 GACATCTAGTTTCTAATCTAAAGCTGGTCTGACACCCCATGTTGGGAGGGCGCCCG 78670
QY 2397 ----- 2397
Db 78671 CTTTTACCCCGACACTGTCTGTCTTTTCCCGTGTCTCACATCTCCCGACATCTCCCGTG 78730
QY 2397 ----- 2397
Db 78731 CTGTGTGACAGGATGACAGCGCGCAGGCCACCATACCTGTGTGGCCAGGGCCTCTGGAA 78790
QY 2397 ----- 2397
Db 78791 GAGTCTAGTGTGGCGTGAACCCCTTGAAGCCAGACAGACAGCTCCCGACTCTTCCAAT 78850
QY 2397 ----- 2397
Db 78851 GTCCGTGACACTTGTGTGTTTCCAAGCAGACACAAAGAGGTGCCCTGTCTGCC 78910
QY 2397 ----- 2397
Db 78911 CTTCTAGGGTCAGGCCAGCCCCGGTCTGGCGCTCTCAGCAGAGGCTTCTAGTCCGGCATA 78970
QY 2397 ----- 2397
Db 78971 GTTGAGTGTCTCTTGGGCAATGCTGTATCCAGCCAGATCTGACATTCCTCAGTGAG 79030
QY 2397 ----- 2397
Db 79031 GGGTACAGTCTGTGGGAGCACCTAAGGAATAGTCAATCTCTCTCATAGTGAATG 79090
QY 2397 ----- 2397
Db 79091 TTATGCTTTCTTACACCAAGGGCTGGCTCTGGCCATCTGGTAGACCTCTTAGCCTCC 79150
QY 2397 ----- 2397
Db 79151 TGGCTCAGGTTTCTCACACTAGTGTCTGTCTGGGGCCCTAGGAGCAGGTGGCTCC 79210
QY 2397 ----- 2397
Db 79211 CCAAGCAGAAATCAGCCCCCACTGCCCTCTCAGTCTGTGGTGGTGTCTTACTGTCAA 79270
QY 2398 ----- GlyGlyGlyLysAlaLys 2404
Db 79271 CCCGCTGACTTGGCCCCCTTCCACTTTGTCCCTCGAGGTGGAGTGGGAAAGCCAAG 79330
QY 2405 ValSerGlyArgProSerSerArgLysAlaLysSerProAlaProGlyLeuAlaSerGly 2424
Db 79331 GTCTTGGCAGACCTAGCAGCGCAAGAACCCAAAGTCGCCAGCAGCCAGGCTAGCTCCGGA 79390
QY 2425 AspArgProProSerValSerValHisSerGluGlyAspCysAsnArgAlaThrPro 2444
Db 79391 GACCGACCCCTCTGTCTCTCAGTACACTCAGAGGGGAGTCAATTCGCCGCAACCA 79450
QY 2445 LeuThrAsnArgValTTPGluAspArgProSerSer 2456
Db 79451 CTCACCAACCTGTGTGGAGGACCGGCCCTCATCTGCAGGTGGGTATCAGTAGGAGTA 79510
QY 2456 ----- 2456
Db 79511 GAGATGTATCCAGGGTTGGGGTTACCTGGGCTACCAAGAAAGAGTCCCTGATCAC 79570
QY 2456 ----- 2456
Db 79571 CACTTAGCAAGAGGATATAGAAAGAAACCTATCAGAGGGTCTGTGTAGTGGCCAGAC 79630

QY 2456 ----- 2456
Db 79631 CTTCCAGGCATGGCTCGTCATACAGGGGAGGCTGCGAGCCTTTCTTGGCTGTGAGGACT 79690
QY 2456 ----- 2456
Db 79691 GTAGGATTTTGACAGGACAGTAAAGGCAGTAGAAGACAGGACAGAGGAGAGCGGAAAGG 79750
QY 2456 ----- 2456
Db 79751 TTTTACTGAGTCCAGTCAATATGGTGTAGGGCTGTCTGAGCACAGAGGCAAGGGAGGAG 79810
QY 2456 ----- 2456
Db 79811 GCCGGTTTGAAGAACTCCAGAGTTAGAGGTCTCTGGCCCAAGAGAGACCCAGGCTCTGTTT 79870
QY 2456 ----- 2456
Db 79871 CTTATATGAAGACGGGTCTGAGTGTCTAGTGGCTTGCAGGCTTGCAGAGCCTCTGCG 79930
QY 2457 ----- AlaGlySerThrProPheProTyrAsnProLeuIleMetArg 2470
Db 79931 CACTCTCCCATCTTTCTCGCAGGGTCCAGGCCATTCCTTACACCTTTGATTATGAGG 79990
QY 2471 LeuGlnAlaGlyValMetAlaSerProProProGlyLeuProAlaGlySerGlyPro 2490
Db 79991 CTACAGGCAGGTGTCTATGGCTTCCCGCCCCCACCCTTGGCGCAGGACGCGGCC 80050
QY 2491 LeuAlaGlyProHisHisAlaThrAspGluProLysProLeuLysSerGlnTyr 2510
Db 80051 CTAGCTGGTCCCCCACCCCTGGGATGAGGAGGCCAAGCCACTGCTGTGTTCACAGTAT 80110
QY 2511 GluThrLeuSerAspSerGlu 2517
Db 80111 GAGACACTCTCGACAGCGAG 80131

RESULT 14
US-10-087-192-652
; Sequence 652, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
; LENGTH: 233380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(233380)
; OTHER INFORMATION: n = A, T, C or G
US-10-087-192-652

Alignment Scores:
Pred. No.: 3,26e-168 Length: 233380
Score: 2951.00 Matches: 1381
Percent Similarity: 17.11% Conservative: 58
Best Local Similarity: 16.42% Mismatches: 238
Query Match: 22.33% Indels: 6744
DB: 12 Gaps: 54

Qy 1263 LeuPro-----LysGlyHisValIleTyrGluGlyLysLysGlyHisVal 1277
 Db 199351 CTGCTGTCTGCTGCCACCGCTGT-----CCTGGCC-CGTGCCCGAGCTC 199397
 Qy 1278 LeuSer-----TyrGluGlyGlyMetSerValThrGlnCysSerLysGlu 1292
 Db 199398 CTACCGAGTGGCTTGTGTGGTTTCCAGGTGGCATGTCTGTGACCCAGTGTCTCCAGGAG 199457
 Qy 1293 AspGlyArgSerSerGlyProProHisGluThrAlaAlaProLysArgThrTyrAsp 1312
 Db 199458 GACGCAAGACAGCTCAGACCCCGCCATGACAGCGCCCGCCCAAGCGCACCTATGAC 199517
 Qy 1313 MetMetGluGlyArgValGlyArgAlaIleSerSerAlaSerIleGlu----- 1328
 Db 199518 ATGATGAGGCGCGGTGGCGAGAGCATCTCTCAGCCAGCATCGAAGGTGATAGCAGG 199577
 Qy 1328 ----- 1328
 Db 199578 GAGGAGACTTCATCTCTCGGTGCCCTCGTGGCGGTGGGGGATGGCTGACCCCGTTT 199637
 Qy 1328 ----- 1328
 Db 199638 TACAGATGGGAAACCGAGGTGGGCTTCTGAGGCTCCATCTGGAGGTAGCCAGGGAC 199697
 Qy 1328 ----- 1328
 Db 199698 CTTCCCGTGGGTCTCTACTCCACCATCATCGTGGGGATGACCACTGGCGGTGTAAAC 199757
 Qy 1328 ----- 1328
 Db 199758 ACTGACCCCTGTACTGCCCCAGTGTGGCTCAGGAGCCAGGATGATGGCTCACCCCT 199817
 Qy 1329 -----GlyLeuMetGlyArgAlaIleProProGluArgHisSerProHisHisLe 1345
 Db 199818 CTCCTACCGAGTCTCATGGCCGCTGTCATCCCGCGAGCGACACAGCCCGCCACCACT 199877
 Qy 1345 uLysGluGlnHisHisIleArgGlySerIleThr----- 1356
 Db 199878 CAAGAGCAGCACCACATCCGCGGTCCATCACACAAGGTACTGCCCTGTTCCTGTCTCC 199937
 Qy 1356 ----- 1356
 Db 199938 CTCGTTGCCCCAACGGGTGTACAGTACGAGCGCGGGAGGAGAGACAGCCAGA 199997
 Qy 1356 ----- 1356
 Db 199998 GTGTGTGGGAATCAGGACAAGTATGCAGAAAGCCTGCAGCACACATGTACATGATCA 200057
 Qy 1356 ----- 1356
 Db 200058 GTACGTGAGCTACGGAGCAAGGTGTCTCTTACTTATTTCAAAACAAAAGCAA 200117
 Qy 1356 ----- 1356
 Db 200118 AATACCACCGATCACCCCTGTGCTTTAGGTGTACATAGCAACTGTCTGTGTGGCA 200177
 Qy 1356 ----- 1356
 Db 200178 CTAACCCAGGTGCCACTCGGTATCGTTTACAGAACATCTCTGGTGAGGCACATCGGATT 200237
 Qy 1356 ----- 1356
 Db 200238 GGGAGAGGTTGGAGAGCTCCGAGAACTCTTTCAGGTTCTCGCGGTGTGTCATGGCACA 200297
 Qy 1356 ----- 1356
 Db 200298 GCCAGTACTGTGAACCTGGCAGCTTTGGGGTTTATTTTATTTTATTTTATTTTGTG 200357
 Qy 1356 ----- 1356
 Db 200358 TTGTTGTGCTTTGTGAGACAGGCTCTATTCTGTGGCCAGGCTGGAGTGCAGTGGCAC 200417
 Qy 1356 ----- 1356

Db 200418 GATCTAGCTCACTGAGCCTCCGCTTTTCAGGCTTAAACAATCTCCACCTTCAGCCTC 200477
 Qy 1356 ----- 1356
 Db 200478 CCAAGTAGCTGGGACCACAGATGCACACCACACACTAGCTAAATTTTGTATTTTGA 200537
 Qy 1356 ----- 1356
 Db 200538 GAGGTGGGTTTACCAATGTTGCCAGGTGGTCTCGAACTCTGAGCTCAAGCTGTCTG 200597
 Qy 1356 ----- 1356
 Db 200598 CTTGCCGACGCCCCCAGAGTGTGGGATTACAGCGGTGAGTACTGCACCCAGCCTGTG 200657
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 Db 200658 GTTTTAGCTTCATGATTTTCATAGTGTCCCGATTTCGTGAGGTGGTTCAGTTAATTTCT 200717
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 Db 200718 TGTTTTATGTGAAGAAGCTGAGGCCAGAGAGGTTCAGATTTCTTGGTCAAGGTACAC 200777
 Qy 1356 ----- 1356
 Db 200778 AGCAAGTGGGATTGAACTCAGGCAGACTAGCTCCAGAACCCACTGGTGTGGAGGTCT 200837
 Qy 1357 -----GlnGlyIlePr 1360
 Db 200838 TGATCGGTCTGGTGGGCGGGCGGTGAGGTTCAGTGTCTCGGCCCGCAGGGATC-CC 200896
 Qy 1360 oArgSerTyrValGluAlaGlnGluAspTyrLeuArgArgGluAlaLysLeuLeuLysAr 1380
 Db 200897 TCGTCTCTAGTGGAGGCACAGAGACTACTCTGCTCGGAGGCCAAGCTCTTAAAGCG 200956
 Qy 1380 gGluGlyThrProProProProProSerArgAspLeuThrGluAlaTyrLysThrGl 1400
 Db 200957 GGAGGCGACGCTCCGCCCCCACCCTTCAGGACCTGACCGAGGCTACAGGCGCTACAGACGA 201016
 Qy 1400 nAlaLeuGlyProLeuLysLeuLysProAlaHisGluGlyLeuValAlaThrValLysGl 1420
 Db 201017 GGCCTTGGGCCCCCTGAGCTGAGCGGCCCTCAGCGGCTGTGTGGCCACGGTGAAGGA 201076
 Qy 1420 uAlaGlyArgSerIleHisGluIleProArgGluLeuArgHisThrProGluLeuPr 1440
 Db 201077 GCGGCGCGCTCCATCCATGATCCGCGCAGAGGCTGCGGCACACGCCCGAGCTGCC 201136
 Qy 1440 oLeuAlaProArgProLeuLysGluGlySerIleThr----- 1452
 Db 201137 CTTGGCGCGCGGCCCTCAAGGAGGGCTCCATCAGCGAGGTATGGCCCGAGGCCAGCA 201196
 Qy 1452 ----- 1452
 Db 201197 CACGGGCCAGTTCTTAGAGGGGTGGCGTGTGGGGCACTGCCCTGGGCTCTCCA 201256
 Qy 1452 ----- 1452
 Db 201257 CATGGGAAACCGAGGCTGAGACCCCTCGGTACCTTACAGTCACCCAGCTGTCTATCAC 201316
 Qy 1452 ----- 1452
 Db 201317 CGGCGCTCAGTGTGCTGTTCAGAGGCTGCGCAGGGGCCACCGAGCTCTGTACCTGATT 201376
 Qy 1452 ----- 1452
 Db 201377 CTACTGAACCTACATTTTCCCATTTTTCAGGAGGAGAACTAGTCCCAGAGAGGCCAG 201436
 Qy 1452 ----- 1452
 Db 201437 GCAGCTTCCAGGCCACAGGACTAAACATAGTGACGAGTAAGTCCGTTGAATCTT 201496
 Qy 1452 ----- 1452

Db	201497	TGTGAGGGTCAGGTGCGGCTGAGGATGTTGCATGGTTCATTGTTTACCCCTAGCA	201556
Qy	1452	-----	1452
Db	201557	ATGCTCTGAGGTGTTTTCTTAATGACTTATTTATTGCTGAGTAAATTGAGTTTCAGA	201616
Qy	1452	-----	1452
Db	201617	GAGGTTCAACGACTCACCCAGAGTCACGACGAAATGCAAGTTGTGAAACCAATTCAGA	201676
Qy	1452	-----	1452
Db	201677	TGTTCTACAGCCGACGATCCACTGCACCCACGAGGTTGCACCAAGAGGCCCA	201736
Qy	1452	-----	1452
Db	201737	GTCCCCCAGCGGCCCCAGCTCAGTAGGGGAAGTTCCGTGCCGATGGTACGAGGACGAG	201796
Qy	1452	-----	1452
Db	201797	GAGCTGTTCCGTGGAAAGCCCCCTGAAGGCCACTGTCTTCCACATGGGCAGAGTGCCT	201856
Qy	1452	-----	1452
Db	201857	CTTGTGAAGGGGAAGGAGAATGGGAGCCACACGCGGCTGTGGGCTGTGAGGCGGAAGG	201916
Qy	1452	-----	1452
Db	201917	ACTGGGTGGGTGTCCTCGGGAGGGTTCCAGCTTGTTAGGAAGTTTGAAGCCAGGAGA	201976
Qy	1452	-----	1452
Db	201977	AGGCAGAAGCAGTAAGATCCTGATTCGAGGGAAGGTTTGGCTCTCAGCCCTTAGGC	202036
Qy	1452	-----	1452
Db	202037	AATTATGGAGTCTTGTGAAGCATCCACGGCATGACCAAGACAGGGTCCAGATTCTAGAAT	202096
Qy	1452	-----	1452
Db	202097	ATTCTTTTGAACAAGGCGAGTTCCCTTCTTACGACAGTAATGAAGACATCCCTAAA	202156
Qy	1452	-----	1452
Db	202157	TAGAGTTTGTGTTGTTGCAAGCCCTAAAGTCCACCATATCAAGTGTCTCCGAAGCCTG	202216
Qy	1452	-----	1452
Db	202217	CTGAAAAGAGCGAGGGACCTGTGTGGCTGTGCTACGAAGGTCCAGTCTGGACTGTGACC	202276
Qy	1452	-----	1452
Db	202277	CCCCCATTTCTCACCATCCTTCTGTCTGGAGGGCAACACCTCAGCCCTGACCTCAGT	202336
Qy	1452	-----	1452
Db	202337	GTCCCTGGGCTGAAAGCCTCAGGGCGGTAGTATTGGGTCTGGGTGCTGACTTTTTCGTG	202396
Qy	1452	-----	1452
Db	202397	CTTTGGCATTTGGTGGGCCATGGAGGGTCCAGGCTGAACAGAGGAATGTTTTTTTACCCAC	202456
Qy	1452	-----	1452
Db	202457	ATGAGGGTGTGGGCTTCTTCTCGCAACTCCAGGGAACCATCAGAGAGCCCACTCG	202516
Qy	1452	-----	1452
Db	202517	CGGCAGGAGAGTTGACTGTTGAACTTTTTACCCCTTCTGCACTCCCCCAGGGAGCGT	202576
Qy	1452	-----	1452
Db	202577	GGGACACAGGGTCAGGCCAGGGTGCAGGGCAGTAAGTAACAAGTGTGCCATCTCAGG	202636
Qy	1452	-----	1452
Db	202637	GTTAGAAAGCCCTCTGTCTCCCTGCTCTGGAGGCATCAGATGCTCACTTCACTTTATA	202696
Qy	1452	-----	1452
Db	202697	GATGACAAACTTTTGTAGGCTCAGAAGGGGATGCAGCTGGTCTGGGCTATGGCTGTGGC	202756
Qy	1453	-----	1463
Db	202757	CAGGGCTAGAGCTTACATCCCTCTGCCCCAGGGCACCCGCTCAAGTACGACACCGGCG	202816
Qy	1463	-----	1483
Db	202817	CGTCCACCACTGGCTCAAAAAGCAGACGTACGCTCCCTCATCGGACGCCCCGCGCGA	202876
Qy	1483	-----	1503
Db	202877	hrPheProValHisProLeuAspValMetalaspAlaArgAlaLeuGluArgAlaC	202936
Qy	1503	-----	1523
Db	202937	GCTTCCACCCGTCACCCGCTGGATGTGTGCGGACGCGCCGACCTGGAACGTGCCT	202996
Qy	1523	-----	1543
Db	202997	GCTACGAGGAGAGCTGAAGCCGCGCAGGACCGCCAGAGCTCGGGGGCTTCCATTG	203056
Qy	1543	-----	1563
Db	203057	ATGAGGACCAAGGGGACCTTTTGGCGGCCACCTCCACAGAGTTTCGCGGTGACACAGC	203116
Qy	1563	-----	1571
Db	203117	GGAGGCCACCGCCGCTCGAGGAGGTGAGTGGGTGTGCATGGCGGTGAGTGGGGTG	203176
Qy	1571	-----	1571
Db	203177	GGCGCTGTCTGGAAGCTGTGCTCCCATCCACATTAGCTTAGTTTGCACCTGGGA	203236
Qy	1571	-----	1571
Db	203237	TATCTCTGCCACCGCTTTCCACCACATCCAAACACCTGCAGGCGCGTGGGCTCTGCCT	203296
Qy	1571	-----	1571
Db	203297	CCGATTCCAAACCTGTCCAACTCTTGCACCTCCAGACACACCGTGGTGTCTCACCTA	203356
Qy	1571	-----	1571
Db	203357	GCTTCCCCCAGCGCCCTCCCTCTTCTGCTGTAATCCACTCTGCAACAGCTACCCGAT	203416
Qy	1571	-----	1571
Db	203417	ACTTCTTAAAAATGCAAAATCATATTATTCACCTTCCCTGCTTTTCATCTTCTAGCAACTT	203476
Qy	1571	-----	1571
Db	203477	CACACATTTTGTATGGCTTGGGGCGCTGCCTGTTGGGGCCCTGCCTGCCTCTCATTC	203536
Qy	1571	-----	1571
Db	203537	AGCGGATTCCTTGGTCTCCCGAGCCCGAGCCCTGGGCCCTTTCTCTTTGTTCCCT	203596
Qy	1571	-----	1571
Db	203597	GGCATGCTTAGCTCGGTCAATTCAAGTCTTTTGTGGGGGCTTTGCGTGGCTCTCTCTCT	203656
Qy	1571	-----	1571
Db	203657	CTGCTGCCATGTCGCGCCCTCCAGATCTTTTACTTAGTGGGTTTCTTTCCATCCCTCAG	203716

Db 205877 AGTCCTCGTGGCACTCAACTACGCTCGGGGTCCCCAGAGTGAGTGGTGGGAGACCAC 205936
Qy 1729 ----- 1729
Db 205937 CTCGGCTGGGTTTGGCCCTATTCCAAAGGACATGGCGGTGCCCTGTGGCCCTCGCGAG 205996
Qy 1729 ----- 1729
Db 205997 GCAGCTAGACCTGGTCAACCTTTGTGGGTCACTTGTGTGAACGACCTGAGTGGGTGCCT 206056
Qy 1729 ----- 1729
Db 206057 GGGTTGTGCGTGTGTGGGTGCTGGTGGCATCTGGTAGTGAGTGCACAGCGTGTGGC 206116
Qy 1729 ----- 1729
Db 206117 TCCTGGTGCATCCTCAGTGGGTGCGTGCATCTGTGTATACTCTTAGGATACAGGGC 206176
Qy 1729 ----- 1729
Db 206177 CTCAGGAGTTAAAGATCAAAATGTGGCGGCACAGTGGCTCATGCTCTGAATCCGAGC 206236
Qy 1729 ----- 1729
Db 206237 ACTTGGGAGGGCAGGAGCGAGTGTGATTAACAAGTCAAGATTCGAGACCAGTCTGACCAA 206296
Qy 1729 ----- 1729
Db 206297 CATGGTAAACCCGCTCTCTCTTAANAATACAAAATTAGCCAGGCATGGTGTGCGCACC 206356
Qy 1729 ----- 1729
Db 206357 TGTGGTCCAGCTACTCACTAGGCTGAGGCAAGAGAAATCACTTGAACCCAGGAGTGGAG 206416
Qy 1729 ----- 1729
Db 206417 GTTACAGTGAAGAGATTTTACCATTCGACTCCAGCTGGGCAACAGGCAAGACTGTG 206476
Qy 1729 ----- 1729
Db 206477 TCTCGAAAAAANAAGATGAATGTGAGGCTGTTGGAGTTGTTCTTTCCTTGGCCTTG 206536
Qy 1729 ----- 1729
Db 206537 TAAACAGCCCAAGCTGCTTTGGGTGCACACGTTCCAGGGCCATCTTCAGAAATGCTTCT 206596
Qy 1729 ----- 1729
Db 206597 GGAATAACCAAGTTCTAGCTGGGGCTCAGCTGGAAAAGCTGAAGTCACTTAAGTATTT 206656
Qy 1729 ----- 1729
Db 206657 TGAACAGTGAAGATTGAATACAGGAATGATTTGTATAGCGTTCAGAGGCTGAAGGGCA 206716
Qy 1729 ----- 1729
Db 206717 CAGAGGCGCTGAGATGGGAACCACTGAGGCGAGCTGCAGGAGATGCCCGGCTCGGGCTT 206776
Qy 1729 ----- 1729
Db 206777 GGGAGCAGAGAGAGAGGTGTAACGAGAGAACCTGAGCATTCAGAAAAGGTTCCATGGC 206836
Qy 1729 ----- 1729
Db 206837 CGGTGTGGAGCGGAGGAGTGCCTGCCACCAGCTCTGCTGGCTCCAGGAGTGTGT 206896
Qy 1729 ----- 1729
Db 206897 GCCGTGCTCTCCAGAGGGTGATCTGGCCGGTGGGAGCCTGGCCTCTCTCCCTCCCTGTG 206956
Qy 1730 -----
Db 206957 GCTACAGCCCTGGCCCAACACCTCCCGCAGGCGCATCATCGACCTGTCCCAAGTCCACACC 207016

Qy 1740 euProValLeuValProThrProGlyThrProAlaThrAlaMetAspArgLeuAlaT 1760
Db 207017 TGCCTGTGCTCGTGGCCCGCCAGACACCCAGCCAGCCAGCCATGCAGCGCCTTGCCCT 207076
Qy 1760 YrLeuProThrAlaProGlnProPheSerSerArgHisSerSerSerProLeuSerPro- 1779
Db 207077 ACCTCCCAACGGGCGCCAGCCCTTCAGCAGCGGCCACAGCAGCTCCCACTCTC-CCCA 207135
Qy 1779 ----- 1779
Db 207136 GGTAGCGCCACTGCCAGTCTGGGTGGGACCCCGGCATCCATGGAGGGCGGTGGGG 207195
Qy 1779 ----- 1779
Db 207196 ATGGGGGGCAGAAAGCCCTGCTCTTTCCACCCAGAAAGACAAAGCCAGGCTCTTCTT 207255
Qy 1780 ----- GlyProThrHisLeuThrL 1787
Db 207256 CGGCCCTGGGGCTGAGTCTCTGCGCTTTTGGGTTTCTTAGGAGGTCCAACACACTTGCAA 207315
Qy 1787 YsProThrThrThrSerSerGluArgGluArgAspArgAspArgGluArgAspArgA 1807
Db 207316 AACCAACCCACAGTCTCTGTCGAGCGGAGAGACCGGATCCGAGCGGACCGG 207375
Qy 1807 spArgGluArgGluLysSerIleLeuThrSerThrThrValGluHisAlaProIleT 1827
Db 207376 ATCGGAGCGGAAAGTCCATCTCACGTCACACGAGCGGTGGAGCACGCCACCTCT 207435
Qy 1827 rpArg----- 1828
Db 207436 GGAG-ACCTGGTAGGGCATCAGAGCCCCACCCCGCTCCGGACTCTTGTGGGCGC 207494
Qy 1829 ----- ProGlyThrGluLysSerSerGlyS 1837
Db 207495 AGAGGCCTCCCTGCTGATGCCACTGCTGCACAGGTACAGACAGCAGCAGCGCA 207554
Qy 1837 erSerGlySerSerGlyGlyGlySerSerSerArgProAlaSerHisSerHisA 1857
Db 207555 GCAGCGCAGCAGCGGGGGGTGGGGCAGCAGCAGCCCGCCCTCCACCTCCCATG 207614
Qy 1857 laHisGlnHisSerProIleSerProArgThrGlnAspAlaLeuGlnGlnArgProServ 1877
Db 207615 CCCACCCAGCATCGCCCATCTCCCTCGACCCAGGATGCCCTCCAGCAGAGACCCAGTG 207674
Qy 1877 alLeuHisenThrGlyMetLysGlyLleIleThrAlaValGluProSerLysProThrV 1897
Db 207675 TGCTTCAACACAGGCATGAAGGGTATCATCCGCTGTGGAGCCCGCAGCAGCCACGG 207734
Qy 1897 alLeu----- 1898
Db 207735 TCCTGAGTGGGCCAGTTGGCATGGGAGGGGGCGGCGAGGTGGATGGTGTGTCAGTA 207794
Qy 1898 ----- 1898
Db 207795 GGAGGATGACAGATAAGAGGATGCTTGTGGGAGGTATATGGAGGTGGGTGGGTGGGC 207854
Qy 1898 ----- 1898
Db 207855 AGATGTGTGGGGTAGAAGAAATAGACTATGTGTGAGTAGTGGATGGGTGGGTGGGT 207914
Qy 1898 ----- 1898
Db 207915 TAGGTGGTGTGTGGGTGAGTGGAGTTAGTTAGTCTGCTGGGTGGATGGATGG 207974
Qy 1898 ----- 1898
Db 207975 ATGGGGGGTGGTGGGTTAGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 208034
Qy 1898 ----- 1898
Db 208035 AGCTGGGTGGGTGGATGGATGGATGGGTGGGTGGATAGGGTTAGGTAGGTGGGTGGG 208094

Db	210255	ATGTGATCGTAGTCTGTTTCTGTAATTAGATGGTAAGATGCTTGCATCCGTTTATGACC	210314
Qy	1898	-----	1898
Db	210315	GCTGTATTACAGTGTCTAGAACAGTGCCTGGCACCTAGTAGTCTTAATCAGAACTTT	210374
Qy	1898	-----	1898
Db	210375	TGGAATGATCAAGGAATGAATGAACGAATGAGTGGATGGGTCAAAACCATGACGCACAG	210434
Qy	1898	-----	1898
Db	210435	AGTCTGCAGGTTTACATCTCAGAGGCGAGTTTCTACTCTGGAGCAGCAGGGGATGTGGAT	210494
Qy	1898	-----	1898
Db	210495	TTATCCAGGCAATGGGACTCATCGAGGGTGTGGAGGAGGAGGCGAGCTCCCATGAC	210554
Qy	1899	-----ArgSerThrSerThrSerSerProValArgProA	1910
Db	210555	TGCCTGACCGCTTCTCTCTCCGCCAGGTCCACCTCCACTCTCACCCGTTGCGCCGG	210614
Qy	1910	laalaThrProProAlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyrP	1930
Db	210615	CTGCCACATTCCCACTGCCACCCACCTGCCACCTGGGCGGCACCCCTCGATGGGGTCTACC	210674
Qy	1930	roThrLeuMetGluProValLeuLeuProLysGluAlaProArgValAlaArgProGluA	1950
Db	210675	CTACCTTCATGGAGCCGCTTGTGTGCCAAGAGGGCCCCCGGTGCGCCGGCCAGAGC	210734
Qy	1950	rgProArgAlaAspThrGlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuG	1970
Db	210735	GGCCCGGAGCAGACACCGGCCATCCCTTCCTCGCAAGCCCGCCAGCCGCTCGCGGGCTGG	210794
Qy	1970	luProAlaSerSerProSerLysGlySerGluProArgProLeuValProProValSerG	1990
Db	210795	AGCCCGCTCTCTCCCGCAGCAAGGGCTCGGAGCCCGCCCTAGTGCCTCTGTCCTG	210854
Qy	1990	lyHisAlaThrIleAlaArgThrProAlaLysAsnLeuAlaProHisAlaSerProA	2010
Db	210855	GCCAGGCCACATCGCCCGCACCCCTCGGAAGAACCCTCGACCTCACACGCCAGCCCGG	210914
Qy	2010	spProProAlaProProAlaSerAlaSerAspProHisArgGluLysThrGlnSerLysP	2030
Db	210915	ACCCGCGCGGCCACCTCGCTCGSCCTCGAGCCGCGCACCGGAAAGACTCAAAGTAAAC	210974
Qy	2030	roPheSerIleGlnGluLeuLeuArgSer-----	2040
Db	210975	CCTTTTCCATCCAGGAACCTGGAACCTCGGTTCTCTGSGGTAAAGACCACCCCTGACAGCGCCA	211034
Qy	2040	-----	2040
Db	211035	CCTTCATAGCGGATTAATCATGCGTCAAAATTGCTACGATAAAGGGGCGGAGAGGAG	211094
Qy	2040	-----	2040
Db	211095	GTGCGCTGGCAACGGCTCCCTCGCGATGTAAGACTTCGCGGCCGACCCACCCCGTC	211154
Qy	2040	-----	2040
Db	211155	TCGTGTGTCAAAGATATTTTTCAGATCTCTGCTTTTACTTTTGGCCCCGCTTTTGT	211214
Qy	2040	-----	2040
Db	211215	GTTGGTTTGTGATTTTGTGTAAGCCCATCCGCTCTCGCGGGTTTGCAGCGCGCTGACG	211274
Qy	2040	-----	2040
Db	211275	ACTACTCGGCGCGCTGCCCTCTGTGTGGGGCGCTCATCATTTTGCACATCAITTT	211334
Qy	2040	-----	2040
Db	211335	ACCATGTTTTTTTTTTTGTGATTTTTTGTCTTTTTTTTCTTTTAAATGAATGGATCTGTGATT	211394
Qy	2040	-----	2040
Db	211395	CTGACTTCGACTGGCGCCCATCTCCCTCTTTGGCCCTGTGTCCAGGAGCAGGATGGG	211454
Qy	2040	-----	2040
Db	211455	GCTCGGAGGGCTCGGGCCTAGCCCCCACCTGCGGCTGCCTGTGATGTGTGCGACTG	211514
Qy	2040	-----	2040
Db	211515	GGGAAAGTGGAGGAGCGCGTGCAGAGGAAGTGAAGCGGGGAGGAGCCTGCGCTGTCT	211574
Qy	2040	-----	2040
Db	211575	GAGGAGGAGCTGGGTCTGGCTCTTGCATCTTGGCCCTGCCAGCCCTGTACCCAGAA	211634
Qy	2040	-----	2040
Db	211635	AAAGGGAGCCCTCTGCCTCTGGACCCCTGCTTGGCCCTAGTTTCATGGCTCTCTCTGT	211694
Qy	2040	-----	2040
Db	211695	TGACTGGGATGGCCGAGGCTATAGCCAGGGGGGGCCCCCGGGAGCCAGGGTCACTCCC	211754
Qy	2040	-----	2040
Db	211755	AGCCACACCCCACTTCTCACTCGGCCCCACACACTCTTCCCGAGAGACCATGTCTGCC	211814
Qy	2040	-----	2040
Db	211815	CCATCTACGCTGGCCTCGCGGCTCCACCACCTGAACCCATCTCTGTCTCTCTTCTTGT	211874
Qy	2040	-----	2040
Db	211875	CCTAAATCTCTCTGTGTCTCCCTCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTCTCT	211934
Qy	2040	-----	2040
Db	211935	CCACCTCTCCCTTGGCCTCCCTGTCTCTCCCAACCCCTCTCTGTCTTACTGTCTTTG	211994
Qy	2040	-----	2040
Db	211995	GGAGCCCAAAACCTTACCCCTAGCTTGGGTTTCCCTTGACCCCGCGGGTCCCAGCCAGC	212054
Qy	2040	-----	2040
Db	212055	TGGAGGGCAGCCCTGCCCCCTCGGGCTCGAAACCCCTGGGCGCGGTGCTGACTCTGCAC	212114
Qy	2041	-----LeuGlyTyrHisGlySerSerTyrSerProGluGlyValGluProVal	2056
Db	212115	CCCCCGCTGCTCTAGTTTACACGCGCAGCAGCTACAGCCCCGAGAGGGGTGGAGCCGTC	212174
Qy	2057	SerProValSerSerProSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGlu	2076
Db	212175	AGCCCTGTGAGTCTACCCAGTCTGACCCAGCACAAGGGGTCTCCCAAGCACCCTGGAAGAG	212234
Qy	2077	LeuAspLysSerHisLeuGluGlyLeuLeuArgProLysGlnPro-----	2091
Db	212235	CTCGACAAGAGCCACCTGGAGGGGAGCTCGGCGCCCAAGCAGCGAGGTACGCCCCACCCA	212294
Qy	2091	-----	2091
Db	212295	GTACCCAGGCCCCGAAGCCCTGCACAGTGAAGACCCTCAAGGCCCATCATGCAGATAG	212354
Qy	2091	-----	2091
Db	212355	GAATAACAGAGGTGCTAAAGGCCAAGGAATTGGCTGTGATCATGAGGCTCAAGAGCATGGG	212414
Qy	2091	-----	2091
Db	212415	GCTGGGATTTGGGCCCGCAGCAGCCCTGGGGGCCAGACACCCCTGACAGCTGTGTCTCT	212474

QY	2092	-----GlyProValIyLeuGlyGlyGluAlaLaHisLeuProHisLeuArgProIe	2109	Db	213555	CAGGCACTCAGTGTACCTTTTACACACAGCCCCCGAGAGACATAGGCAGCATTTCTCC	213614
Db	212475	GCCTGACGGCCCGCTGAAGCTTGGCGGAGGCGGCCACCTCCACACACTCTGGCGCGCT	212534	QY	2204	-----	2204
QY	2109	uProGluSerGlnProSerSerSerProLeuLeuGlnThrAlaProGlyValIyLeuGlyHi	2129	Db	213615	CATTTTCAGATGAGAAACTAAGCCTTGAGAGTGAATTCACTTCCCCACAGGGGCAC	213674
Db	212535	GCCTGAGAGCCAGCCCTCGTCCAGCGCCGCTGTCTCCAGACCGCCCGAGGGGTCAAAGTCA	212594	QY	2204	-----	2204
QY	2129	sGlnArgValIyThrLeuAlaGlnHisIleSer	2140	Db	213675	AGTCAGTAGGTGACAGAGGGGGATTGTTCCAGGGCTGTATATTAGAGAGAGCCTTTC	213734
Db	212595	CCAGCGGTGTCACTCTGGCCCGACACATCAGTGTAACTACGGTTCCTCTGCTGTCT	212654	QY	2204	-----	2204
QY	2140	-----	2140	Db	213735	CACACATGCACACCCACACACATGCGCACACACACATGCGCACACCCGCGCACATGCGCA	213794
Db	212655	TGTCACCTTTGCACCTGGGGGACACAGCGCTGAGAGGGGATGGGAAACCCACAGCCCT	212714	QY	2204	-----	2204
QY	2140	-----	2140	Db	213795	CCCGCACACACACAGTGCACACCCACACACATGCGGCGGCACACATGCGACACCCGCA	213854
Db	212715	TCTGTCTGGCGGGTGGCTGGGGGATCCAGGSCATGGCGCTGGGGGATCCAGGGCGTG	212774	QY	2204	-----	2204
QY	2140	-----	2140	Db	213855	CACATGCGGCACACACATGCGCGCACACACACATGCGCACACCCGCGCACACATGCGCA	213914
Db	212775	GGTGAGGGTGAGTCCCAAAGCCCGAGCACCGGCACCATCACCGCCCTTAATCCATGG	212834	QY	2204	-----	2204
QY	2140	-----	2140	Db	213915	CACACACATGCACACCCCGCACACAGGCGCACCCGCGCACACCCCTGTAGACAGGCACA	213974
Db	212835	GAGGAGCCTGTGATGCGAGCGGATGGCATCTTCAGGGGCAATGAGGCCTTCCTGGTGGCC	212894	QY	2204	-----	2204
QY	2140	-----	2140	Db	213975	TGCATGTCTACGCACACTCCCACTCCACCCCGCCCCCACCCTGGTGAACC	214034
Db	212895	CAGGTTTCTCAGTGTCTATGGCTGGTCTCATCAGCCATCTGCCAATACCACTGGGAC	212954	QY	2204	-----	2204
QY	2140	-----	2140	Db	214035	GTGGGGCTCTGGGGGTCAAAAGAGAAAGAGAGAGGGGGGCCCTGAGTCCAGGGTGAAG	214094
Db	212955	CGCTGACACAGCCCCACTCCCATGCACACTGGGACACGGAGGCCAGAGGGTGGCGGC	213014	QY	2204	-----	2204
QY	2140	-----	2140	Db	214095	GAGGCGTTTTTGTGGGGCGGGGGGGTAAATGTGTGCGGAGACAGACATGGCAAGACA	214154
Db	213015	AGGTCCACAGTCACCAGGAAGCTGGGCCACCACAGGATTTGTGCCCGAGCTCCGTCTAG	213074	QY	2204	-----	2204
QY	2140	-----	2140	Db	214155	GCAGGACATCTTTGGGGGCGAGTGTGTAGTGGCACTGGGGTACAAACAGAAATTCAGAG	214214
Db	213075	CCCCCCCCCAGAGGTTCTGTCCAGGAGTGTGCTGACTCTGGGGCCCCCCCCA	213134	QY	2204	-----	2204
QY	2141	-----GluValIleThrGlnAspTyrThrArgHisHisProGlnLeuSerA	2157	Db	214215	CAGGGGTCAATAAACTGTGGCCCATGGCCAGATCTAGCCCGGGCCCTCTGTTGTACAA	214274
Db	213135	CTTGGCTGCAGGAGGTCTATCACAGGACTACACCCCGCACCCACAGCAGCTCAGCG	213194	QY	2204	-----	2204
QY	2157	laProLeuProAlaProLeuTyrSerPheProGlyAlaSerCysProValIyLeuAspLeuA	2177	Db	214275	TTCATGAACATAAAAAATGATTTTACATTTTAAAGGGTGTGTTTAAAAAATAAAAA	214334
Db	213195	CACCCCTGCCCGCCCCCTTACTCTTCCCTGGGGCCAGCTGCGCCCTCTGGACCTCC	213254	QY	2204	-----	2204
QY	2177	rgArgProSerAspLeuTyrLeuProProProAspHisGlyAlaProAlaArgGlys	2197	Db	214335	TGATAACGATACATGCCAGAGATTACTTGTGTGCGAAAAATGCCATAAACGTTTATGATTT	214394
Db	213255	GCCGCCACCCAGTGACCTACTCTACTCTCCCGCCCGGACCATGGTGCCCGCCCGTGGCT	213314	QY	2204	-----	2204
QY	2197	erProHisSerGluGlyIyIys	2204	Db	214395	GGCCACGTACAGGAAAGCGTGTGGGGCCCTGGTTTAGAGTGGAGGGAGGGTGCGCCCC	214454
Db	213315	CCCCCCACAGCGAAGGGGCAAGAGGTGAGCGAGGGATGGGGGTGCCTCTTGTGCTGGTCAG	213374	QY	2205	-----ArgSerProGluPro	2209
QY	2204	-----	2204	Db	214455	TCAGTAGGAGACCTCTGACCCACATCTGGGGCCCTTTCTCCATCCAGGTCTCCAGAGCCA	214514
Db	213375	CCGGCGGAGGCTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	213434	QY	2210	AsnLysThrSerValIyLeuGlyGlyGluAspGlyIleGluProValSerProProGlu	2229
QY	2204	-----	2204	Db	214515	AACAAGACGTCTTGGGTGTGGGTGAGGACGGTATTGAACCTGTGTCCACCGGAG	214574
Db	213435	GAGGCCCGCTGGTGCCATTGCACAGGCAAGAAATGGAGGCTCCAGGAGATGGGGAGTC	213494	QY	2230	GlyMetThrGluProGlyHisSerArgSerAlaValTyrProLeuLeuTyrArgAspGly	2249
QY	2204	-----	2204	Db	214575	GGCATGACGAGGACGAGGCGACTCCCGGAGTGCTGTGTACCGCTGCTGTACCGGATGGG	214634
Db	213495	ACAGCGGATACATACGAATAATAGCTGATAAAGTACATGCTGTGCTCAGTGGGTTC	213554	QY	2250	GluGlnThrGluProSer	2255
QY	2204	-----	2204				

Db	214635	GAACAGACGAGCCAG-GTACTTCTGTGGGCACATGGCTGCCCCCGGAGTGTCTGGT	214693
Qy	2255	-----	2255
Db	214694	ATCCTTGGCCATCCTTTGGCCCCCAGTCCACCGTGGTGCCATGTGGAGAGTGACAAGGCA	214753
Qy	2255	-----	2255
Db	214754	CAGGGCTCAGTGGTGACCTCAAGCCTGCGCAAGCAGTTTACCAACTTTGGGGGTGTGA	214813
Qy	2255	-----	2255
Db	214814	TACATGCCACCCCTCCCTGGGGAGACCTCAGTGGTAGCTTTCCATGTCTTTGGGGTGGGAT	214873
Qy	2255	-----	2255
Db	214874	CTCAGCTGGACAGCCCCCGTTGACAGCCCTCTTGAACCTCTAAGAAATAATGACTA	214933
Qy	2255	-----	2255
Db	214934	GGTGTCTGGGCCAGACCGGGGCGATGGGTGAGGTGGGACCTCAGAAGGAAGCTGGGCC	214993
Qy	2255	-----	2255
Db	214994	CGTGCCCTTGGGGAAGGCGATGATCGGAACCCAAATTTTCAGTCTCTGGGGCTCTTTGAG	215053
Qy	2255	-----	2255
Db	215054	AGSGTCAGGCTGGAGCAGTGGTTCAGAGGAGCCACCAGCAGCAGCGGTCTCCCAAG	215113
Qy	2255	-----	2255
Db	215114	ACACCCCTAGCCCGGAGCGGTGAACCGCAGAGGAGATTTTCAGAGCCGTGATCTTCTA	215173
Qy	2255	-----	2255
Db	215174	CCAGGCAGGGGATGCAGCGCTGGGGCGGTGAAGCTTGCTTCCAAATGTCTAAGGCATC	215233
Qy	2255	-----	2255
Db	215234	TCAGTGGTGAGTTCCCATCATCAAGGATGCAAGCTCGGCACCAAGTGAGTGTGT	215293
Qy	2256	-----ArgMetGlySerIysSerProGlyAsnThrSerGlnPro	2268
Db	215294	GAGGTGTTTGCATCTCACAGCAGGATGGGTCTCAAGTCTCCAGGCAACACACAGCGCG	215353
Qy	2269	ProAlaPheSerIysLeuThrGluSerAsnSerAlaMetValIysSerIysGln	2288
Db	215354	CCAGCCTTCTTCAGCAAGCTGACCGAGAGCAACTCCGCCATGGTCAAGTCCAAAGAAGCAA	215413
Qy	2289	GluIleAsnLysLysLeuAsnThrHisAsnArgAsnGluProGluTyrAsn-	2305
Db	215414	GAGATCAACAAGAAGCTGAACACCACACCGGATGAGCTGATACAG-TAAGGGGCC	215472
Qy	2305	-----	2305
Db	215473	TGCAGGCTCCCGGGAAGCATGGGCCACAGGTGGGGGTGGCCTCGCTGGGCGAGTGG	215532
Qy	2305	-----	2305
Db	215533	AGCGGCCAGTGGCAGAAACCACGGTGCACCTTCGAAAGCTAAGTGGCCCTGCTGACCA	215592
Qy	2305	-----	2305
Db	215593	CTCCCCCAGGCCCTTTGGCTCACAATTTGGGGAGCCCCAGGGCAGTTTCTTGATTGCT	215652
Qy	2305	-----	2305
Db	215653	GGGCTTTCCATAGAGCTTACTGCGCAGAGAATAAGCACCAGCACATAGTAGTGCCT	215712
Qy	2305	-----	2305
Db	215713	AGTGAATACCTGCATGAATACTGGGACCAAGGGGTGGATCCCTCCACACAAGGGCGGG	215772

Qy	2305	-----	2305
Db	215773	CGCTCCACACTCAGCACCTGTGTGGCTTTGCACCCATTGACGTGTGTGGGTATGA	215832
Qy	2305	-----	2305
Db	215833	ACGCCCACTCTCTTTCCAGTCCCTTAGCACAGCGCTGGCAGTTAGCAGATCCACCAG	215892
Qy	2305	-----	2305
Db	215893	GAATACGTGAGTGGTGGGCAAAATAAAGAAATCTGTACAGTCCCCGACCCCAAGAAGCCT	215952
Qy	2305	-----	2305
Db	215953	CATCTGCCAGGAAGTTTGGACAAATCACAGATGCTTTTCCCTTCTGGGGCTGGAGTAG	216012
Qy	2305	-----	2305
Db	216013	AAACCTTGACAGATAGTCACTGGCTTGC CGGCACGTGGTGCCTCATGCCCTATAGGCCACGA	216072
Qy	2305	-----	2305
Db	216073	CTTTGGGAGGATGAGGAGGAGGATTCCTTGAAGCCAGGAGTTTCGAGACCAGTCTGTGCA	216132
Qy	2305	-----	2305
Db	216133	ACATAGCAAGACCCCATCTCTACAAAAAACTTTAAAAACAGGCACACACCTATAGTCCA	216192
Qy	2305	-----	2305
Db	216193	AGCTCTGGGAGGCTGAGATAGGAGGATTTCTTGAGCCTCGGAGGTCAAGGCTGCAGTG	216252
Qy	2305	-----	2305
Db	216253	AGCTATGATCACACCTGACCTCCAGCTTGGCAACAGAGCAAGACACTGTCTTAAAAA	216312
Qy	2305	-----	2305
Db	216313	AAAAAAATCTCTGACCCAGGCTGGTAACCTCCAGGCCCTGTAAAGTGCAGTCCAGGAA	216372
Qy	2305	-----	2305
Db	216373	CCGTAGCATCAGCATCCCGAGGTACTGGTTAGAAATGCAGGCCCTTGGCCAGGCGCGT	216432
Qy	2305	-----	2305
Db	216433	GGCTTACGCTGTAAATCCCAGCACTTTGGGAGGTCAAGGCGGTGGATCATATGAGTCA	216492
Qy	2305	-----	2305
Db	216493	GGAGTTTGAGACCAGCCTGACCAACATGGTGAACCCCGTCTCTACTAAAAATACAAAA	216552
Qy	2305	-----	2305
Db	216553	TTAGCCAGGCGTGGTGGCGATGTCTGTAAACCCAGCTACTCGGAGGCTGAGCAGGAG	216612
Qy	2305	-----	2305
Db	216613	AATCACTTGAACCTGGAGGCGGAGGTTCAGGAGCCGAGATTGCAACAACCTGCACCTCCA	216672
Qy	2305	-----	2305
Db	216673	GCCTGGCAACAGACGAGACTCTATCTCAAAAAAATAAAAAAAGAAATGCAGACGCT	216732
Qy	2305	-----	2305
Db	216733	TGGCCCTGTCCAGGCGCTGCTGCATGAGAACCCTGCAATGCACAAGTTTCCCGAGGTGATG	216792
Qy	2305	-----	2305
Db	216793	CCAGCACACCTGGCCTGGACCAACACGGGACTGTGTAGGGCAGGTAATTTCCAGAGACCTGG	216852

[illegible]

QY	2324	LeuMetThrTyrArgSerGlnAlaValGlnGluHisAlaSerThrAsnMetGlyLeuGlu	2343
DB	220153	CTTATGACCTATAGAAGCCAGCGGTGCAGGAACAATGCAGCACCAATGCGGGCTGGAG	220212
QY	2344	AlaIleIleArgLysAlaLeuMetGlyLysTyrAspGlnTTPGluGluSerProLeu	2363
DB	220213	GCCATATTAGAAAGGCACTCATGGTTAAATATGACCAGTGGGAAGAGTCCCGCGCGCTC	220272
QY	2364	SerAlaAsnAlaPheAsnProLeuAsnAlaSerAlaSerLeuProAlaAlaMetProfile	2383
DB	220273	AGCGCCAAATGCTTTTAACCCCTCTGAATGCCAGTGCAGCTGCCCGCTGCTATGCCCAT	220332
QY	2384	ThrAlaAlaAspGlyArgSerAspHisnhrLeuThrSerPro	2397
DB	220333	ACCCTGTGACGACGAGGTGACACACACTCACCTGCCAGGTCTGAGGCCACCCCC	220392
QY	2397	-----	2397
DB	220393	GCCCGCCCCGTCTGTCCCCACCCCGGTGTGATTAATCCTCGCTCTCCGCGCTCCTC	220452
QY	2397	-----	2397
DB	220453	TGCAACCCCCCTCTCGAGCTTTGGAGCTGTGACTTTATTTTGTGGTGTGTGACCTC	220512
QY	2397	-----	2397
DB	220513	GTTCTGGAGTTTGTATATCTGAAGCTGGGCTGCACACCCCCCAAGTGTCTGTACCTCTGC	220572
QY	2397	-----	2397
DB	220573	CCCCAGCCCCGGCCCTCTGCCCACTAGGCCGGAAGCGCTGCCCGCTCCCTCGGACACT	220632
QY	2397	-----	2397
DB	220633	CACACTGTCTCGCCCCCCCAGTCTCTCCCGCTTCTCCCTGCGGGGACCCGGCTTCTTG	220692
QY	2397	-----	2397
DB	220693	GCCCATCTGTCTCTTGGGGGAGAGAGGCTGGAGTGAAGCCCAACCCACACTGTGTGGA	220752
QY	2397	-----	2397
DB	220753	CAGGGGAATGCAGCAGGCCCTGTGCTCAGCATCTGCAGGCCCACTATGTGTCTCAGC	220812
QY	2397	-----	2397
DB	220813	TGCCCTTAGCCTTGGTGGGAGAGCCAGGGTCTGTCTCAGCCCTGGGAGTCAGGAGC	220872
QY	2397	-----	2397
DB	220873	CTTAGGGTCAAGCCTGGTTCCCATCAATACCTCTGTATCGGGCAGGGAGCTGAGGAG	220932
QY	2397	-----	2397
DB	220933	AGATTGCAGTTGTCCAACTGGACATGAGGCCCAAGAGACTTCTGGAGCCTCTGTGG	220992
QY	2397	-----	2397
DB	220993	GGGTCAAGCCTGGCTCAGGGGTCTGTACTTCTCTGCACGGGGCTGGATCCTGCTAGC	221052
QY	2397	-----	2397
DB	221053	CTTAGCATGGTCTGGGGCCAGCTCAAACTGGAAGCCAGCTTCATGCTTAGGGTTCCA	221112
QY	2397	-----	2397
DB	221113	GCCCTGGGGCTGGGTGCTGCAGGACAGCCAGGGGGCTATTGCAACACAGACAGACT	221172
QY	2397	-----	2397
DB	221173	TTAGCCACTCCCCCTGCCAGCAGAAACTATCTCCACCCTCCAGGCTCATGGCTGGCCA	221232

Qy	316	IleGluAenAenProAArgArgAlaLysGluSerLysValArgGluTyrTyrGluLys	335
Db	646	ATAGAAATAATCTCGAGGAAGCTAAAGAAAGCAAAACAAGCGAATACTATGAAAG	705
Qy	336	GlnPheProGluIleArgLysGlnArgGluLeuGlnGluArgMetGlnSerArgValGly	355
Db	706	CAGTTTCCAGAAATTCGAAACAAGAGAACAGCAAGAAAGATTTCAG---CGAGTTGGG	762
Qy	356	GlnArgGlySerGlyLeuSerMetSerAlaAlaArgSerGluHisGluValSerGluIle	375
Db	763	CAGAGGGAGCTGCTCTTTGAGCCACCATGCTAGGAGTGAGCAATGAGATTTCTGAAATT	822
Qy	376	IleAspGlyLeuSerGluGlnGlnAenLeuLysGlnMetArgGlnLeuAlaValIle	395
Db	823	ATTGATGGCTCTCTGAGCAGAAAGTAATGAGAAACAAATGCGCGAGCTCTCTGTGATT	882
Qy	396	ProMetLeuTyrAspAlaAspGlnGlnArgIleLysPheIleAenMetAsnGlyLeu	415
Db	883	CCACCTATGATGTTGATGTCAGAACAAAGACGAGTCAAGTTCATTAACATGAATGGCGCT	942
Qy	416	MetAlaAspProMetLysValTyrLysAspArgGlnValMetAsnMetTrpSerGluGln	435
Db	943	ATGGAGAGCCCTATGAAGTGTAATAGATAGCGCGTTTATGAATGTTTGGACTGACCAT	1002
Qy	436	GluLysGluThrPheArgGluLysPheMetGlnHisProLysAenPheGlyLeuIleAla	455
Db	1003	GAAGAGGAGATCTTTAAGGACAAGTTTATCCAGCATCCAAAAACTTTGGACTAAATTGCA	1062
Qy	456	SerPheLeuGluArgLysThrValAlaGluCysValLeuTyrTyrLeuThrLysLys	475
Db	1063	TCATACTTGGAGAGAAAGAGTGTTCCTGATTGTTGTTTGTATTACTATTAAACCAAGAA	1122
Qy	476	AsnGluAenTyrLysSerLeuValArgArgSerTyr---ArgArgArgGlyLysSerGln	494
Db	1123	AATGAGAATTATAAAGCCCTCGTCAGAAAGAAATTTATGGAAACCCAGGCGAGAAACCG	1182
Qy	495	GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln	514
Db	1183	CAAAATTCGACCCCTCGCAAGAGAAAAGTAGAAGAAAAGAAAGAG-----GATAAA	1236
Qy	515	SerSerGlnGluLysAspGluLysGluLysGluLysGluAlaGluLysGluGluGlu	534
Db	1237	CGCAAAAAACAGAAAAAAGAGAGAGAAAGAAAGATGAAGAGGAAAAAGATGAAAA	1296
Qy	535	LysProGluValGluAenAspLysGluAspLeuLysGluLysThrAspAspThrSer	554
Db	1297	GAAGACTCCAAAGAAAAATACAAGGAA-----AAGGACAAGATAGATGGTACAGCA	1347
Qy	555	GlyGluAspAenAspGluLysGluAlaValAlaSerLysGlyArgLysThrAlaAsnSer	574
Db	1348	---GAAGAAACTGAGGAAGAGAGCAGCACCCCGGGGGCGAAGAGCTGCCAACAGT	1404
Qy	575	GlnGlyArgArgLysGlyArgIleThrArgSerMetAlaAenGluAlaAenSerGluGlu	594
Db	1405	CAGGGCCGCGTAAGGGCCGATCACCAGGTCCATGATCAAAACGAAGCTGCAGCTGCCAGT	1464
Qy	595	AlaIleThrProGlnGlnSer-----AlaGluLeu	604
Db	1465	GCTGCAGCCGCGCGGTACTGTGAAGAGCCCCACCACCTCTGCCACCGCCACAGAAACCC	1524
Qy	605	AlaSerMetGluLeuAenGluSerSerArgTrpThrGluGluGluMetGluThrAlaLys	624
Db	1525	ATTCTACAGAGCTGTGGAGACCTCTCGATGGACAGAGAGAAATGGAAATGCTCTAAA	1584
Qy	625	LysGlyLeuLeuGluHisGlyArgAsnTrpSerAlaIleArgMetValGlySerLys	644
Db	1585	AAAGGCTAGTAGAACATGTCGTAACTGGCAGCAATTCGTAATAATGGTGGGAACGAAA	1644
Qy	645	ThrValSerGlnCysLysAenPheTyrPheAsnTyrLysArgGlnAenLeuAspGlu	664
Db	1645	AGTGAAGCTCAATGTAAAAAATTCTATTATTAACTATAAAGGGCGACCAATCTTGCAAC	1704

Qy	665	IleLeuGlnGlnHisIysLeuLysMetGluLysGluArgAsnAlaArgArgLysLys	684
Db	1705	CTCTTACAGCAGCATAAACAGAAAACCTTCACGAAAACCTCGTGAAGACGAGATGTGTCT	1764
Qy	685	LysAlaProAlaAlaAlaSerGluGluAlaAlaPheProProValValGluAspGluGlu	704
Db	1765	CAATGTGAAGTGTGCGTCTCCACTGTTTCGCT-----CAGGAGGATGAAGAT	1812
Qy	705	MetGluAlaSerGlyValSerGlyAsnGluGluGluMetValGluGluAlaGluAlaLeu	724
Db	1813	ATTGAACCTCC-----NATGAGAGAGAAATCCAGAGACACGCGAGGT--	1857
Qy	725	HisAlaSerGlyAsnGluValProArgGlyGluCysSerGlyProAlaThrValAsnAsn	744
Db	1858	-----CGAGAAAAT	1866
Qy	745	SerSerAspThrGluSerIleProSerProHis---ThrGluAlaAlaLysAspThrGly	763
Db	1867	AGTTCTGATACAGAAAGTGTCTCTTCTCCTACCAGTGAAGCTGTCAAG-----	1917
Qy	764	GlnAsnGlyProLysProProAlaThrLeuGlyAlaAspGlyProProGlyProPro	783
Db	1918	-----CCACCGAGGAC	1929
Qy	784	ThrProProArgArgThrSerArgAlaProIleGluProThrProLaserGluAlaThr	803
Db	1930	AGTCTGAAAATGCTACTTCTCGAGGAAACACAGAACCTCGCGTTGAGCTTGAG----	1983
Qy	804	GlyAlaProThrProProProAlaPro---ProSerProSer---AlaProProProVal	821
Db	1984	-----CCCCACCGAAACTGCACCAGTACATCTCCCTCTTACGAGTTCACAGTACA	2037
Qy	822	ValProLysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	837
Db	2038	AAACCAGCTGAAGATGAAGTGTGGAGACCCAGCTGAATGACAGCATCAGTCTGAGACA	2097
Qy	838	-----GluGluGlyGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	844
Db	2098	GCAGAGCAGATGGATGTAGATCAGCAGGACACAGTGTGAAGAGGTTCTGTTTGTGAT	2157
Qy	845	ProProAlaAlaGluGluLeuAlaAlaAspThrGlyLysAlaGluProValLysSer	864
Db	2158	CCCCACCCGCTACCAAA-----GCTGACTCTGTGGACGTTGAAGTGAAGGTGCCAGAA	2211
Qy	865	GluCysThrGluGluAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	884
Db	2212	AACCATGCATCTAAAGTTGAAGTGATATACCAAGAAGAGACTTGGATGAGGCC---	2268
Qy	885	AlaThrAlaGluGlyAlaLeuLysAlaGluLysGluGlyGlySerGlyArgAlaThr	904
Db	2269	-----AGTGAGAAGTGGAACTTGAACCTAGAGATGAAGATTTGGTG	2304
Qy	905	ThrAlaLysSerSerGlyAla-----ProGln---AspSerAspSerSerAla	919
Db	2305	GTAGCTCAGCAAAATAAATGCCAAAGGCCCGACCCCGAGTCAGACAAATGATTCAGTGCC	2364
Qy	920	ThrCysSerAlaAspGluValAspGluAlaGluGlyLysAspLysAsnArgLeuLeuSer	939
Db	2365	ACGTGCAGCGCTGATGAG-----GATGTGGATGGAGAGCCAGAGAGCCAGAAATGTTT	2418
Qy	940	Pro-----ArgProSerLeuLeuThrProThrGlyAspProArgAlaAsnAlaSer	956
Db	2419	CCTATGGACTCAAGACCTTCACCTGTTAAACCCCACTGGATCTTACTCGTC---TCATCT	2475
Qy	957	ProGlnLys-----ProLeuAspLeuLysGlnLeuLysGlnArgAlaAlaAlaLeuPro	974
Db	2476	CCGTTAAACCAAAATCCACTGGATCTGCCACAGCTTCAGCATCGAGCTGCTGTATCCCA	2535
Qy	975	ProIle-----	976
Db	2536	CCAATGGTATCTGCGACCCCATGTAACATACCAATGGGAACCCAGTGCAGCGCTATGCT	2595
Qy	977	-----GlnValThrLysValHisGluProProArgGluAspAlaAlaProThr	992

[illegible]

QY	1016	GlySerSerProArgGlyLysSerArgSerProAlaProProAlaAspLysGluAlaPhe	1035	
Db	191495	AGTACCCT-CCTGTGGCAAC-----CCCTGGAGTAGCTCACGGGCCGTG	191538	
QY	1036	AlaAlaGluAlaGlnLysLeuProGlyAspProProCys-----	1048	
Db	191539	GGCCACAGAAAGAAATGGTTGAAAGCCCGAGAGCCTGTCAAGTGTCTATTCCCTCTGAG	191598	
QY	1049	---TriPThrSerGlyLeuPro-----PheProValProPro	1059	
Db	191599	GGGTGGG-CGGGGGCTCCCGGGCTCAITTCGTATAGTCTGGACTCGGCTGCCCTGGA	191657	
QY	1060	ArgGluValIleLys-----AlaSerPro-----HisAlaProAspProSer	1073	
Db	191658	AGGAGAGCCCTGGCTAGTAGTGGCAAGCCAGCGCTTTTACCTTCGGGGCCACCTCGCTCT	191717	
QY	1074	AlaPheSerTyrAlaProProGly-----HisProLeuPro-LeuGlyLeuHisAspTh	1091	
Db	191718	GTTCACTCTCTGCTGCTCGGGGAGCAGTGGCCGCCATGTAGGCTCTCTTGGCCT	191777	
QY	1091	rAlaArgProValLeuProArgProProThrIleSerAsnProProProLeuIleSerSe	1111	
Db	191778	GGCGAGGCCCTCGCCACCCCTCACCACTGGCTGCAAC-----	191817	
QY	1111	rAlaLysHisProSerValLeuGluArgGlnIleGlyAlaIleSerGlnGlyMetSerVa	1131	
Db	191818	---ACACACCTCTCCGTGCACAGCAGACTGTGTGGTGGACACTCACATGCACATCGGC	191873	
QY	1131	Gln-----	1132	
Db	191874	ACAGTTCTGGGTGCACAGTGTATACATAAAGCCGTGTACTGCTGCACCCCTGGT	191933	
QY	1133	-----LeuHisValProTy	1137	
Db	191934	ACATGTGTGTACATGACCCACTTAGTTCTCAGCAGCCAGGCTCACGTGATGGCCAC	191993	
QY	1137	rSerGluHisAlaLysAlaProValGlyProValThrMetGlyLeuPro-----	1153	
Db	191994	ATCCACTCTCGCACACACAGACCCGTGCCAGTGTGCATGCTGCTCTGCTGCCACAC	192053	
QY	1154	-----LeuProMetAspPro--	1158	
Db	192054	GTCCACACACTGCTGATGTATCGGTGCACAGCGTGTCTGCTGCTGCCCGCACCTCCACT	192113	
QY	1159	-----LysLysLeuAlaPro-----	1163	
Db	192114	CTGCTGTATCGGTGCACGCGTGTCTGCTGCCACACATCCACACTGCTGTGTATGT	192173	
QY	1164	-----PheSerGlyValLysGlnGluLeuSerProArgGl	1176	
Db	192174	ATCGGTGCAGTGTGCTCTGCTGCCACACATCCACACTGCTGTATGCTCTTGTCT	192233	
QY	1176	YcInAla-----GlyProProGluSer-----LeuGlyValProThrAl	1189	
Db	192234	ACGTGCATGTGTGCACCTTGTTCACGCCCATGTGCGCACCCGTGGGTGTGGACAGA	192293	
QY	1189	aGlnGluAlaSerValLeuArgGlyThrAlaLeu-----GlySerValProGlyGlySe	1207	
Db	192294	CTCACGTGCTCATGTGTGCAGGACACCCCTTGTTCACAGACAGACACCTCGAGGGC	192353	
QY	1207	rIleThrLysGlyIleProSerThrArgValProSerAspSerAlaIleThrTyrArgGl	1227	
Db	192354	TAGGTACAGGTGCAGGAGGCTGCCCTGTCATCTCCACCGTGCACCCCTCGAAAAG	192413	
QY	1227	ySerIleThrHisGlyThrProAlaAspValLeuTyrLysGlyThrIleThrArgIleIl	1247	
Db	192414	CTCCTGG-----GTCTGTGGCAGGCC-----CA	192440	
QY	1247	eGlyGluAspSerProSerArgLeuAspArgGlyArgGluAspSer-----	1262	
Db	192441	GGGCTGCAGGCTGCCAGCTCCCTCTGGAGGCTCGGCTGTGAGGCTTTGTGACGGGCC	192500	
QY	1263	-----LeuProLysGlyHisValIle-----Ty	1270	
Db	192501	AGCATGGAAGCACGTGCTGCTCTGCTACCGGCTCTGCTGCTGCCACCGTG	192560	
QY	1270	rGluGlyLysLysGlyHisValIleuSer-----TyrGluGlyGlyMetSe	1285	
Db	192561	GTCTCGGGCCCGTCCCGAGCTCTCACCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	192620	
QY	1285	rValThrGlnCysSerLysGluAspGlyArgSerSerSerGlyProProHisGluThrAl	1305	
Db	192621	TGTACCCAGTGTCTTCCAGGAGGACGCGAGAGCAGCTCAGGACCCCCCATGAGAGCGC	192680	
QY	1305	aAlaProLysArgThrTyrAspMetMetGluGlyArgValGlyArgAlaIleSerSerAl	1325	
Db	192681	CGCCCCAAGCGCACTATGACATGATGGAGGCGGTGGGAGAGCCATCTCTCTCAGC	192740	
QY	1325	AsrIleGlu-----	1328	
Db	192741	CAGCATCGAAGGTGATAGCAGGAGGAGACTTCACTCTCTCGGTGCCCTCGTGGCGGT	192800	
QY	1328	-----	1328	
Db	192801	GGGGGATGGTGCACCCCGTTTTACAGATGGGAAACCGAGGCTGGGCTTCTGAGGCTC	192860	
QY	1328	-----	1328	
Db	192861	CATCTGAGGTAGCGCAGGACCTTCCGCTGTGTGGTCTCTACTCCACCATCATCTGGGG	192920	
QY	1328	-----	1328	
Db	192921	ATGACCACTGGCGGCTGTAAACACTGACCTGTCACCTGCCAGTGTGGCTCAGGGAGC	192980	
QY	1329	-----GlyLeuMetGlyArgAlaIleProProG	1338	
Db	192981	CACGGAATGATGGCTCACCTCTCTACCCAGGCTCTCATGGGCGGTGCCATCCCGCGG	193040	
QY	1338	luArgHisSerProHisIleLysGluGlnHisIleArgGlySerIleThr-----	1356	
Db	193041	AGCGACACAGCCCCCACCACTCAAGAGACACACATCCCGGGGTCCATCACACAAG	193100	
QY	1356	-----	1356	
Db	193101	GTACTGCCCTGTTCCTGCTCCTGTTGCCCCCAAGGGTGTACAGTCAAGCAAGGAGGCT	193160	
QY	1356	-----	1356	
Db	193161	GGGAGGAGAGACACAGCCAGAGTGTGTGGAACTCAGGACAAATGCAAGAAAGGCT	193220	
QY	1356	-----	1356	
Db	193221	GCAGCACATGTATCATGTATGATGAGTACGAGTACGAGCAAGGGTGTCTCTTACTTAT	193280	
QY	1356	-----	1356	
Db	193281	TCAAAACAAAACAAAAGCAAAATACCACCGATCACCCCTGTGTCTTTAGGTGTACAT	193340	
QY	1356	-----	1356	
Db	193341	AGCAACTGTCTGTGTGTGCACTAACCCAGGTGCCACCTGCGTATCGTTTACAGAAC	193400	
QY	1356	-----	1356	
Db	193401	TCCTGTGAGGCATGCGATTGGAGAGGCTTGGAGAGGCTCCGAGAACTCTTTTACAGTT	193460	
QY	1356	-----	1356	
Db	193461	CTCGCGCTGTCCATGGCACAGCCAGCTACTGTGAATTTGGCAGCTTTTGGGTTTAT	193520	
QY	1356	-----	1356	
Db	193521	TTTTTATTTTTTATTTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	193580	
QY	1356	-----	1356	

Db	193581	CCAGGTGGAGTCAGTGGCAGCATCTCAGCTCACTGACGCTCCGGCTTTACGGCTTAA	193640
Qy	1356	-----	1356
Db	193641	ACAATCTCCCACTTACGCTCCCAAGTAGCTGGGACACAGATGCACACACACATCT	193700
Qy	1356	-----	1356
Db	193701	AGCTAAATTTTGTATTTTGTAGAGTGGGTTTACCATGTTGCCAGGCTGCTCGA	193760
Qy	1356	-----	1356
Db	193761	ACTCCTGAGCTCAAGCTGTGCTGCGCAGCCCCCAGAGATGTGGATTACAGCGGT	193820
Qy	1356	-----	1356
Db	193821	GAGCTACTGCACCCAGCTGTGGTTTATGCTTCATGATTTCATAGTGTCCCGACTTGT	193880
Qy	1356	-----	1356
Db	193881	GAGGTGGTTCAGTTAATATCTTGTGTTATGTGAAGAAGCTGAGGCCACAGAGGTCA	193940
Qy	1356	-----	1356
Db	193941	GATTCCTGGTCAAGGTCACACAGCAAGTGGGATTTGAATCAGGCAGACTAGTCCAG	194000
Qy	1356	-----	1356
Db	194001	AACCCACTGGTGTGGAGCTCTTGATGGTCTGGGTGGGGCGGCGTGAGGTCAGTGC	194060
Qy	1357	-----	1357
Db	194061	GTGCGGCCCGCAGGGATC-CCTCGTCTACGTGGAGGCACAGGAGACTACCTGGCTC	194119
Qy	1373	-----	1373
Db	194120	GGGAGGCCAGCTCTTAAGCGGAGGCGCGCTCCGCCCCCAGCCCTCAGCGGACC	194179
Qy	1393	-----	1393
Db	194180	TGACCGAGGCTCAAGACGAGCGCCCTGGGCCCCCTGAGCTGAAGCGGCCCATGAG	194239
Qy	1413	-----	1413
Db	194240	GCCTGTGGCCACCGTGAAGAGGCGGCGCTCCATCCATGATCCCGCGCAGGAGC	194299
Qy	1433	-----	1433
Db	194300	TGCGGCACACGCCCGAGCTGCCCCCTGGCCCGCGCGCTCAAGGAGGGCTCCATCAGC	194359
Qy	1452	-----	1452
Db	194360	AGGTATGCCCGCCAGGCACACAGGCCCGCAGTTCTTAGGAGGGTGGCGGTGCTGG	194419
Qy	1452	-----	1452
Db	194420	GGCACTGCCCTGGGCTCTCCACATGGGGAACCGAGGCTGAGAGCCCTCGCTACCTTA	194479
Qy	1452	-----	1452
Db	194480	CAGTACCCAGCTGCTCATCACCGGCTCAGCTGTGCTGTTCACAGGCTGGCGAGGG	194539
Qy	1452	-----	1452
Db	194540	GCACCGGCTCCTGACCTGATTCTACTGAACCTACATGTTTCCCATTTCTCAGGGAGGA	194599
Qy	1452	-----	1452
Db	194600	AACTAGTCCAGAGAGGCCAGGCGCTTCCAGGCCACAGGACTAAACATAGTACGA	194659
Qy	1452	-----	1452
Db	194660	GTAATGCTCCCTCGTTGAATCTTTGTGAGGGTCCAGGTGCGGCTGAGGATGTTGCATGG	194719
Qy	1452	-----	1452
Db	194720	TTCAATGTTTCAACCCCTAGCAATGCTCTGAGGTGCTTTCTTAATGACCTTATTTATT	194779
Qy	1452	-----	1452
Db	194780	GCTGAGTAAATTTGAGGTTTCAGAGAGGTTCAACGACTCACCCAGAGTCAAGCAAAATGC	194839
Qy	1452	-----	1452
Db	194840	AGTTGTGAACCCAAATTCAGATGTTCTTACAGCCGAGCATCCACTGCACCCACACGCA	194899
Qy	1452	-----	1452
Db	194900	GGTTGCACCAAGAGAGGCCAGTCCCCCAGGCGGCCAGCTCAGTAGGGGAAGTTCC	194959
Qy	1452	-----	1452
Db	194960	GTGCGATGGTACGAGGACGAGGAGTGTTCGGTGGAAAGCCCCCTGAAGGCCACTGTCT	195019
Qy	1452	-----	1452
Db	195020	TCCACATGGGAGAGGTGGCTCTTGTGAAGGGGAAGAGATGGAGCCACACGGGGC	195079
Qy	1452	-----	1452
Db	195080	TGTGGGCTGTGAGCGGAAGGACTGGGGTGGGTGTCCCGGAGGGGTTCCAGCTTGTAG	195139
Qy	1452	-----	1452
Db	195140	GAAGGTTTGAAGCCAGGAGGAGGAGCAGTAAGATCCCTGATTGTCAGGGGAAGG	195199
Qy	1452	-----	1452
Db	195200	GTTTGGCTCTCAGCCCCCTAGCAATATATGAGTCTTGGAAAGCATCCACCGCATGACCA	195259
Qy	1452	-----	1452
Db	195260	GACAGGTCAGATTCTAGAATATCTTTTGAACCAAGGCGAGTTCCTCTTACGA	195319
Qy	1452	-----	1452
Db	195320	CAGTAATGAAGACATCCCTAAATAGAGTGTGTTGTTGCAAAAGCCCTAAAGTCCCA	195379
Qy	1452	-----	1452
Db	195380	TATCAAGTGTCTCGAAGCCCTGTGAAAAGAGGAGGGGACCTGGTGGCTGGCTACGA	195439
Qy	1452	-----	1452
Db	195440	GGTCCAGTCTGGACTGTGACCCCCCATTTCTCACCATCTTCTGTCTGGAGGGCAA	195499
Qy	1452	-----	1452
Db	195500	ACACCTCAGCCCTGACCTCAGTGTCTCGGGCTGAAAAGCTCAGGGCGGGTAGTATGG	195559
Qy	1452	-----	1452
Db	195560	GTCGGGTGCTGACTTTTCTGCTTGGCATTTGGGTGGCCCATGAGGGTCCAGGCTGAA	195619
Qy	1452	-----	1452
Db	195620	CAGAGGAATCTTTTATACCCACATGAGGGTGTGGGCTTCTTCTCGCAACTCCAGGA	195679
Qy	1452	-----	1452
Db	195680	CCATCAGAGAGCCACCATCTCGGCGCAGGAGAGTTGACTGTTGAATTTTACCCCTTT	195739
Qy	1452	-----	1452
Db	195740	CTGACGTCCCCCAGGAGCGTGGGGACACAGGCTCAGGGCCAGGGTCCGAGGGCAGTAA	195799

Qy	1732	IleAspLeuSerGlnValProHisLeuProValLeuValProThrProGlyThrPro	1751
Db	200179	ATCGACCTGTCCCAAGTGCACACACTGCTGCTGCTGGCCCCGACACCAGGCACCCC	200238
Qy	1752	AlaThrAlaMetAspArgLeuAlaTyrlLeuProThrAlaProGlnProPheSerSerArg	1771
Db	200239	GCCACGCCCATGGACCGCCTTGCTTACCTCCCAACCGGCCACGCCCTTCAGCAGCGC	200298
Qy	1772	HisSerSerProLeuSerPro-----	1779
Db	200299	CACAGCAGCTCCCACTCTC-CCAGGTAGGCCACTGCCAGTCTGGGTGGGACCCC	200357
Qy	1779	-----	1779
Db	200358	GGCATCCATGGAGCGCTGGGGATGGCGGGCAGAAGCCCTGCTCTTTTCCACCC	200417
Qy	1779	-----	1779
Db	200418	CAGAAAGCAAAGCCAGGCTCTTCTTGGCCCTGGGCTGAGTCTCTGGCCTTTGGGTTTC	200477
Qy	1780	---GlyGlyProThrHisLeuThrLysProThrThrThrSerSerSerGluArgGluArg	1798
Db	200478	CTAGGAGGTCCAACACTTGACAAAACCAACCAACCACTGCTCGTCCGAGCGGAGCGA	200537
Qy	1799	AspArgAspArgGluArgAspArgAspArgGluArgGluLysSerIleLeuThrSerThr	1818
Db	200538	GACCGGGATCCAGAGCGGAGCCGGGATCGGGAGCGGGAAAAAGTCCATCTCACGTCACCC	200597
Qy	1819	ThrThrValGluHisAlaProIleTrpArpProGly-----	1830
Db	200598	ACGACGGTGGAGCAGCAGCACCCATCTGGAGACCTGGTAGGGCATCAGAGCCCCACCCCC	200657
Qy	1831	-----	1831
Db	200658	GCTCCGGGACTCTTGTGGGCGCGCAAGAGCCTCCCCCTGCTGATGCCACTGACTG-TCA	200716
Qy	1835	SerGly-----SerSerGlySerSerGlyGlyGlyGlyGlySerSerSerArgPro	1851
Db	200717	CCNGGTACAGACAGCAGCAGCGGCGAGCAGCGCGGGGTGGGGGCGAGCAGCAGCCGCCCC	200776
Qy	1852	AlaSerHisSerHisAlaHisGlnHisSerProIleSerProArgThrGlnAspAlaLeu	1871
Db	200777	GCCTCCACTCCCATGCCCCACAGCAGCTGCCCCATCTCCCTCGACCCAGGATGCCCTC	200836
Qy	1872	GlnGlnArgProSerValLeuHisAsnThrGlyMetLysGlyIleIleThrAlaValGlu	1891
Db	200837	CAGCAGACCCAGTGTGCTTCACAACACAGGCATGAAGGTATCATCACCCTGTGGAG	200896
Qy	1892	ProSerLysProThrValLeu-----	1898
Db	200897	CCCAGCAGCCCCACCGTCTT-GAGGTGGCCAGGTGGCATGGGGAGGGGGCGGCAGG	200955
Qy	1898	-----	1898
Db	200956	TGGATGGGTGTCAGTAGGAGGATGAGCAGATAAGAGGATGCTTGGTGGGAGGTATATGG	201015
Qy	1898	-----	1898
Db	201016	GAGGTGGGTGGGTGGGCAGATGTGTGGGGTAGAAGAATAGACTATGTGTGAGTAGTGGA	201075
Qy	1898	-----	1898
Db	201076	TGGGTGGGTGTCGGGTAGTGGGTGTGTGGGTGAGTGGGTGAGTGGGTAGTGGGTG	201135
Qy	1898	-----	1898
Db	201136	GGTGGATGGATGGATGGGGGGGTGTGCGGGTTAGTGGGTGGGTGGGTGAGTGGAA	201195
Qy	1898	-----	1898
Db	201196	AGATAGATGGCTGGTGGTGGATGGGTGGATGGATGATCAGGTTTGGTAGGTAGGTGG	201255
Qy	1898	-----	1898
Db	201256	GTGGGTGGAAGGATAGATGGCCGGTTAGCCAGATAGTGGTTGGGTAGGTGGGTAGGT	201315
Qy	1898	-----	1898
Db	201316	GGGTCAGTGGGAGGATAGATGTTAGGTTAGCTGGGTGGGTGGGTGGATGGATGGGTGGG	201375
Qy	1898	-----	1898
Db	201376	TGATAGGTTAGGTAGGTAGTGGTGGGTGGGTGGAGGATAGATAGCTGGGTTAGCTGGGTG	201435
Qy	1898	-----	1898
Db	201436	GATGATGGGTGGGTGCTCACGTTAGGTAGGTAAGTAGTGGGCAAAAGATAGATGGCC	201495
Qy	1898	-----	1898
Db	201496	AAGTTAGTAAATAGGTGGGTGGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGTAGGT	201555
Qy	1898	-----	1898
Db	201556	ACCCCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	201615
Qy	1898	-----	1898
Db	201616	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	201675
Qy	1898	-----	1898
Db	201676	ATCCAGAAACTGATGCAAGAGTGGGTTTTCCATGGCCTTTAGGAAGCTCCACCTCTGTG	201735
Qy	1898	-----	1898
Db	201736	GCTTTCAGAGTACAGCCCCCTCTGCTGCTTTTCATGGGCTGGCATTTAGTGTCTGCCA	201795
Qy	1898	-----	1898
Db	201796	CTTTTCCAGGCACATGGTCAAGCTGTCAATGGAGCTACCATTCTGGGGTTTGGAGAACA	201855
Qy	1898	-----	1898
Db	201856	ATGGCCCTCTTCTCACAGCTTCACTAGTCCCTAACTGGGACTCTGTTTGGGGCTCTGA	201915
Qy	1898	-----	1898
Db	201916	CTCTACATTTCCCTTCTGCACTGCCCTTAACAAAGGTTCTCCATGAGGCTCTGCCCTGC	201975
Qy	1898	-----	1898
Db	201976	AGCAAACTTCTGCTGGATATCCTGGCATTCCTATCATCTCATCTAGGCTGAGG	202035
Qy	1898	-----	1898
Db	202036	ATTCAAATCCACAACCTTTATGCTGCTGTGCACTGCGAGGCTTAACACCAATGAAGCCA	202095
Qy	1898	-----	1898
Db	202096	CTAAGTCTTATGGGTGACACCCCTATCGAGCAGTGGGTTAACATATATCTGAGCCCTTT	202155
Qy	1898	-----	1898
Db	202156	AGCTACAACCTGGACTTTGAGTGGGTGGGACACAGGAGCAATGTCCCATGGATGTGAGG	202215
Qy	1898	-----	1898
Db	202216	GCAGCAGTCCCTGGGCATGGACAATGAACCAATCTTCTCTCCAAGACCTCTGGGCTTG	202275
Qy	1898	-----	1898
Db	202276	TGATGGGAGGGCTGCTACAAAGTTCTTGAAATATCTTCAAGGCATTTTCCACATTTGT	202335
Qy	1898	-----	1898

Db	202336	CTTGGCTATTAAACATTCAGCAATGTTACATATGCAAAATTTCTGTAGATGGCTTGAATTAC	202395
Qy	1898	-----	1898
Db	202396	TCCCATAAATGGGGTATTCTTTTCTAGTCATGGACAGACTGCAATATTCTTAAACTTTT	202455
Qy	1898	-----	1898
Db	202456	TATGCCCTGCTTCCCTTTAAATATAACTCTCAGTTTCAGACATCTCATTGCTCACACAT	202515
Qy	1898	-----	1898
Db	202516	ATGACCATATGCTGTTAGAACATCCAGGACATCTTCAATGCTTTTGTCTCAGTGTG	202575
Qy	1898	-----	1898
Db	202576	TGGGGGTGACTACAAATACATTTCATGCTTATATACAATGCATTTGAGGTTGAGGCATGTA	202635
Qy	1898	-----	1898
Db	202636	AAATACTAAGGCACGTGTGTATGTTGTTGTGCATGATACTGTAACCTCTGTCTCTG	202695
Qy	1898	-----	1898
Db	202696	AAACAGTACAGGAACAGGATGTGTGATAGGAGTGTGAAGACAGCATCTTAAGAAATG	202755
Qy	1898	-----	1898
Db	202756	TGGTTGATGCTTCAGATGAATAAATAAGTCCATATGACCTCATGCTGCCCCCAATAGC	202815
Qy	1898	-----	1898
Db	202816	CACCTGTTGATGAATTATACTCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	202875
Qy	1898	-----	1898
Db	202876	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	202935
Qy	1898	-----	1898
Db	202936	NNNGTTAGTCTCCTTCAGGATCTTGTACGCGCGCCTGTGGTCTCTTATCATTTG	202995
Qy	1898	-----	1898
Db	202996	CTTGTCTGTAAGGATTTTATTCTCTCTTGTCTTATGAAGTTTAGTTAGCTGATGTA	203055
Qy	1898	-----	1898
Db	203056	AATTCAGTAGAAAAATTAATTTCTTTAAGAAATCTTAAATATTGCCCCCCACTGTTTTCT	203115
Qy	1898	-----	1898
Db	203116	GACTCATAGGGTTTCTGCAGAGATCGGTGTTAGTCTGATGAGCTTCCCTTGTGGTA	203175
Qy	1898	-----	1898
Db	203176	ACCTGACCTTCTCTGCGTCTCTTAACTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	203235
Qy	1898	-----	1898
Db	203236	CTGATGATTATGTCCTTGGGTTACCTTCTCTAGGAGTGTCTTTGTGTCTCTGTA	203295
Qy	1898	-----	1898
Db	203296	TTTCCCGAATTTGAATTTTGGCCTGTCTTGTAGTTGGGAAGTCTCTCTGGATAATAT	203355
Qy	1898	-----	1898
Db	203356	CCTGAAGAGTGTTTTCCAACTTGTCTTCCATTTCTCCCATCACTTTTCAGGTACACCAAGC	203415
Qy	1898	-----	1898
Db	203416	AAATGTAGATTGGTCTTTTACATAGTCCCATATTTTCTTGAGGCTTTGTCTTCTCTT	203475
Qy	1898	-----	1898
Db	203476	TTCAATCTTTTCTCTAAATCTTGTGTTTTCACATTTTATTTATTAATTTGATCTTCAGTC	203535
Qy	1898	-----	1898
Db	203536	GCTGATATCCTTTCTTCCACTTGATTGCTATTGGCTATTGACACATGTGTATATCTACGA	203595
Qy	1898	-----	1898
Db	203596	AGTTCTCATGCTGTGTTTTCAGCTCTATCAAGTCATTTATTTCTACTCTCAAACTGGTT	203655
Qy	1898	-----	1898
Db	203656	ATTCTAGTTAGCAATTTATTTAATCTTTTCAAGTTCTTAGCTTCTTGCATTGGGTT	203715
Qy	1898	-----	1898
Db	203716	AGAACATGCTCTTTTAGCTCAGAGAGTTTGTATTACCCACCTTCTGAAGCCTACTTCT	203775
Qy	1898	-----	1898
Db	203776	GTCAAATTCATAAACTCATTTCTCCATCCAGTTTGTTCCTTGTGCGGAGGAGTTGTGA	203835
Qy	1898	-----	1898
Db	203836	TCCTATGAAGAGAGAGACATCTGTGTTTGGGAAATTTTCAGTCCTTTTGCACCTGTTT	203895
Qy	1898	-----	1898
Db	203896	CTCCCATCTTCATGGATTATCTACCTTGGTCTTTGATGTTGGTGACCTTTGGATGG	203955
Qy	1898	-----	1898
Db	203956	GTCTCTGAGTGGACATCTTCTGTGTGATGTGATTTATTCCTTTCTGTTGTAGTTT	204015
Qy	1898	-----	1898
Db	204016	CTTCTTAACAGTCTGGCCCTCTGCTGAGGTTTGTGTCAGTTTGTGAGGTCCACTCC	204075
Qy	1898	-----	1898
Db	204076	AGACTCTGTTTGTCTGGGTATCACTAGCGAGGCTGCAGAACAAAGATTGCTGCTG	204135
Qy	1898	-----	1898
Db	204136	TTCTTCTCTGCAAGCTTCTCCAGAGGACACCCACAGCTGCCAGCGGAGCTCTT	204195
Qy	1898	-----	1898
Db	204196	TTGTATGAGGTGTCTGTTGGCCCCCACTGGGAGGTGTCTCCAGTCAGGCAATGTGGGT	204255
Qy	1898	-----	1898
Db	204256	CAGGACCGCTTGGAGGAGGAGTCTGTGATGAATTTCTCANNNNNNNNNNNNNNNNN	204315
Qy	1898	-----	1898
Db	204316	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	204375
Qy	1898	-----	1898
Db	204376	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	204435
Qy	1898	-----	1898
Db	204436	TGCACCAATATGACCAGCAATTTCTTTGATATTTTTTAAGAGATGGATCTTACTACG	204495
Qy	1898	-----	1898
Db	204496	TGTTACAGGCTCAGCCTCCCAAGTAGCTGGGATTTATAGTAAAGACCAACACACCAGC	204555
Qy	1898	-----	1898

QY	1898	-----	1898
Db	204556	CCAAATTAGATTGTTCTTAAGAGATATTCTGACCAGCCTTTAAATATCTAATCATAG	204615
QY	1898	-----	1898
Db	204616	TCACCTACTGAAAAACGGTCTTGACTTCTGTATTAGTTTCCTATTGCTGCTGAACACA	204675
QY	1898	-----	1898
Db	204676	AACCTTAGTGGCTTAAATAGCACAAATGTATTGCTGACAAATCTCGAGGTGAGAACTTA	204735
QY	1898	-----	1898
Db	204736	GAATGTCTCTACCTGGCTAAACCAAGATGCCAGGCTGGTCTCTTCTGAAATGCCTAG	204795
QY	1898	-----	1898
Db	204796	CGGGAAATTCAATTGCTTGCTTTTACCACCTTCTTGGAGAAGGAGTCTACATGCTTTT	204855
QY	1898	-----	1898
Db	204856	TTGGCGCATGCCCTCTTCTGTATTCAAAGCTAGCAATGCTGGTGGATCTTTCTCAAA	204915
QY	1898	-----	1898
Db	204916	CTCTATCACTGACCTGCGCTCTGCTCTTCTACTTTTAAGTACCTTGTGATTCCATTGGGA	204975
QY	1898	-----	1898
Db	204976	TTGCTGATAACTCAGGATAGTCTCTTATTTAATCACTCAACTGTTTAAACAACATTAAAC	205035
QY	1898	-----	1898
Db	205036	TCGCTCTTTAACTCTGGTTTCTCTTGCTATGTGACATAAGACACTTACAGTTTTGAGG	205095
QY	1898	-----	1898
Db	205096	GTTAGATGTGGACATCTGTGAAGGAGACATTATCTCTCTACCATTGCTTCCAGTAT	205155
QY	1898	-----	1898
Db	205156	CTAGCAAAACCATCTGCTGCTGGTCTTTCTACTGCTGGGTGCGAATTTACTCTCCA	205215
QY	1898	-----	1898
Db	205216	GCCTTACCCCAAGACCTCATGTGATGTGCGCTCGAGTTCACACACACCATCCATC	205275
QY	1898	-----	1898
Db	205276	CAGATCCCCCAACACACCCCACTCACACAGCTCATAGCATTTGTTCTTGCAATTTATC	205335
QY	1898	-----	1898
Db	205336	TTCTTTTGATGTTCTCTTATTCACGCTGCTCCCTTTACTCACCAAGATGAATCACTC	205395
QY	1898	-----	1898
Db	205396	TGTTCACTCTCGACTTATAGCAATGCATCTTCTCCATGAAGCTTTTCCCTTAACCTT	205455
QY	1898	-----	1898
Db	205456	TTCCCTCTGGATGTTTCATATCATATGTTTGTACCTCTCTGTANNNNNNNNNNNNNN	205515
QY	1898	-----	1898
Db	205516	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	205575
QY	1898	-----	1898
Db	205576	NNNNNNNNNNNNNNNNNNNNNTTGAATTGTGGGTGTTGCTGGCGTTAAGTAGTAG	205635
QY	1898	-----	1898

Db	205636	GTAAGTGGGGAAGAAAGATGCCAGATTAGCCAATGTGAAGAAAGATGGGGGG	205695
QY	1898	-----	1898
Db	205696	TGNTAAGTTAGGAAGGTAGGGGGGTGGGGAGAGATATAGACGCTGGCTTAGNTGGGGG	205755
QY	1898	-----	1898
Db	205756	GTGGATGGTGGTGGTAGGGTTAGGGAGGTAGNTGGTGGGTGAGAGTATAGATGGCTG	205815
QY	1898	-----	1898
Db	205816	GGTTAGCTGGTGGTGGTGGATGGGTGGGTGGGTAGGGTTAGGTGGATGGAATGGA	205875
QY	1898	-----	1898
Db	205876	TGTTGGATGAGTAATTTGTGGGATGAGTGGATGGAGCCCCCAGTGGATGGACGATGAT	205935
QY	1898	-----	1898
Db	205936	TGGCGGTGGGATGAGTAGATGGGAGGTGTTGTTGGTTTGAGAAATAGAATCTGTGGAG	205995
QY	1898	-----	1898
Db	205996	GGAGAGACTGAATGGGACTGTGAGAAAGACTTTCGCGTCCCCCACATTTAGCAAGC	206055
QY	1898	-----	1898
Db	206056	CAGCAAGGAAAGAGGTGTCCTCTTGGCTGGACAAAGTCCCAAGTTTCTCTGAGATGG	206115
QY	1898	-----	1898
Db	206116	AGAGGCCCTGAGTGCCTCTGTGTACACACACTCCAGAGACTGTGGGAGAGCTGCTTC	206175
QY	1898	-----	1898
Db	206176	ACCAGGGGGTGGGTGCACACCTCAACACCTTCCCTGCCCGGAACCTTTTTTTTTTT	206235
QY	1898	-----	1898
Db	206236	TTTTTTGATGAGTTGTACTCTGTGCGCCAGGCTGGAGTGCAGTACGATCTCTGCTT	206295
QY	1898	-----	1898
Db	206296	ACTGCAACCTCCACCTCCTGGGTTCAAGTGAATCTCCTGCTCAGCTCCCAAGTAGCTG	206355
QY	1898	-----	1898
Db	206356	CAGTTACAGCACGTGCAACCAACCCGGCTAATTTTATATTTTATAGTAAATCGGT	206415
QY	1898	-----	1898
Db	206416	TTCAACACGTTGGCCAGGCTGTCTCAAACTCTGACCTCAAGTGAATCTGCTGCTCAG	206475
QY	1898	-----	1898
Db	206476	CTCCCCAAAGTGGCGGATTAAGGCGTGGCCACCGCACTCAGCCTCCAGGACCTATTT	206535
QY	1898	-----	1898
Db	206536	AGAGGCAACTTACTCTCTCCAAATGAATTTTCATTCAAAAAAGTACTTGTGCCCCA	206595
QY	1898	-----	1898
Db	206596	GCCGCTTGGATGCTGAAGTACATCTCCCTTAATCATTTTCAATTATGAAAAATGGC	206655
QY	1898	-----	1898
Db	206656	ATCGTTTCCCAAAAGCAGTGGCGACTTTGTCACCCCTGACTCAGACCCAGCGTGCATG	206715
QY	1898	-----	1898

D	206716	AAGCACTAATCCCTGGCTGTGGGAGCAGAGGTTCCGCACACAGGCTCTGTGGGATATGCC	206775	Qy	1996	ArgThrProAlaLysAsnLeuAlaProHisAlaSerProAspProProAlaProPro	2015
Qy	1898	-----	1898	D	207856	CGCACCCCTCGAAGAACCTTCACACCTTCACACGACCGACCGCCGCGCCACCT	207915
D	206776	CGTGACAGCCGATTCAAATAATATATGAGAAAACAGAGTGCTGCCCACTGCCCGCTCAT	206835	Qy	2016	AlaSerAlaSerAspProHisArgGluLysThrGlnSerLysProPheSerIleGlnGlu	2035
Qy	1898	-----	1898	D	207916	GCCTCGGCCTCGACCCGACCGGAAAGACTCAAAGTAAACCTTTTTCATCCAGAA	207975
D	206836	GAATGAGGCTCTGGGAGTAGAGTTAGCGAGAGATGGGGTGCCCCATGGAACGCAGG	206895	Qy	2036	LeuGluLeuArgSer	2040
Qy	1898	-----	1898	D	207976	CTGGAATCTCCGTCTCTGGGTAAGACCACTTCACAGCGGCACCTTCATAGACCGAT	208035
D	206896	GCTCCGGGAAGCCACGTGGGTGGAGCAGCGCGCTCCTGTTCAGACCCAGCCCTGTGCA	206955	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208036	ATCATGGTCAAAATTGCTCACGATAAAGGGCGCGAGAGAGTGCGTGGCCACCGC	208095
D	206956	GGGCGAGCTGCCCCAGCTTCTCACTCACAGAGCTGGGAACAGAGCTTCTCTGTCT	207015	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208096	TCCCTCGCATGTAAGACTTCGCGCCGACCCACCCGCTCTCGTGTGTCAAAGATAT	208155
D	207016	CAACGCCACCTGGCGCGCCCTGGCATCCTTCCCTTGTCTCTCACTCCTCACGTGG	207075	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208156	TTTCAGATCTCTGCTTTTACTTTTGGCCCCGGTTTTTTTGTGTGTTTGTGTATTT	208215
D	207076	CTTTTTTAGCTCTTCCGGTATCTCTGAGCAGCCAGCTCCCTCATGTGCCCCCTCCCTGA	207135	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208216	GTTTTGAAGCCATCCGCTCGCGGTTTGACGCGCTGACGACTACTCGGCGCGGCC	208275
D	207136	AGACCTCCTAGCCTGCTCAGCTTCTTGGCGTCTCTCTGCTGCTGCTCACTTACTACC	207195	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208276	TGCCCTCTGTTTGGGGGCGCTCATCATTTTGACATCATTTTACCATGTTTTTTTTT	208335
D	207196	TCCACACAGTTACCAGGCTCTGTAGAGCTTGGGATATCTGTTAATGTATCTGTCTGT	207255	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208336	TTGGAATTTTGTCTTTTTCCTTTAATGAATGAATCTGTGATCTTGACTGCGCC	208395
D	207256	TTTCTGAATTAGATGGTAAGATGCTTGATCCGTTTATGACCGCTGTATTTCAGATGT	207315	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208396	CCCATCTCCCTCTTTGGCGCTGTGCCAGGAGCAGGATGGGGCTCGGGAGGCTCGG	208455
D	207316	TAGAACAGTGCTGGCACCTAGTAGTGTCTTAATCAGAAAGTTTGGAAATGATGCAAGAA	207375	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208456	GCCTACGCCCCACCTCGCGGCTCCTGTGATGTCTCGACTTGGGGAAGTGGAGCAGG	208515
D	207376	TGAATGAACGAATCAGTGGGATGGTCAAACCATGACGACAGAGTCTGGCAGGTTACAG	207435	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208516	CGGTGAAGGAGAAGCTGAGCGCGGGGCGAGGAACTCTGCTGTCTGAGGAGAGCTGGGTCT	208575
D	207436	TCAGGAGGCGAGTTTCACTCTGGGAGCAGCAGGGGATGTGGATTTATCCAGGCAATGG	207495	Qy	2040	-----	2040
Qy	1898	-----	1898	D	208576	GGCTCTTGCACTTGCCCTGTCCCGAGCCCTGTACCCAGAAAAGGGGAGCCCTCTGC	208635
D	207496	GGACTCATCGAGGTGTGGAGGAAGAGGGGAGCTCCCATGACTGCTGACCGCTTCTC	207555	Qy	2040	-----	2040
Qy	1899	-----ArgSerThrSerThrSerSerProValArgProAlaAlaThrPheProPro	1915	D	208636	CTCTGGACCCCTGCTTGGGCCCTAGTTTCATGGCTCTCTCTGTTGGACTGGGATGGCGA	208695
D	207556	TCCTCCCGCCAGGTCACCTCCACCTCTCTCACCCGTTGCGCGGCTGCCACATTCACCT	207615	Qy	2040	-----	2040
Qy	1916	AlaThrHisCysProLeuGlyGlyThrLeuAspGlyValTyProThrLeuMetGluPro	1935	D	208696	GGCTATAGCCACGCGGGGGGCCCGGGAGCCAGGGTCACTCCCGACCCACCCCACTTC	208755
D	207616	GCCACCCACTGCCCACTGGGCGGCACCTCTCGATGGGGTCTACCCCTACCTCATGGAGCC	207675	Qy	2040	-----	2040
Qy	1936	ValLeuLeuProLysGluAlaProArgValAlaArgProGluArgProArgAlaAspThr	1955	D	208756	TCACTCGCCCCACACACTCTCTCCCGAGAGACCCATGCTGCCCCCATCTCACGCTGGCC	208815
D	207676	GTCCTGTGCCCAAGAGGCCCGCCCGGTCCCGCCAGAGCGCGCCCGGAGACACCC	207735	Qy	2040	-----	2040
Qy	1956	GlyHisAlaPheLeuAlaLysProProAlaArgSerGlyLeuGluProAlaSerSerPro	1975	D	208816	TCGCGCGGCTCCACACACTGAACCCATCTCTGTCCCTTCTTGCTTAATCTCTCTCTGTG	208875
D	207736	GGCCATGCTTCTTCGCCAAGCCCCCAGCCGCTCCGSGCTGGAGCCCGCTCTCCCCC	207795	Qy	2040	-----	2040
Qy	1976	SerLysGlySerGluProArgProLeuValProProValSerGlyHisAlaThrIleAla	1995	D	208876	TCTCCCTCTCTGTGTGTCTGTGTCGGGGTCTGTGCATCTCTCTCCACTCTCCCTTGCGC	208935
D	207796	AGCAAGGGCTCGGAGCCCGGCCCTTAGTGCTCTCTGTCTCTGCGCCAGCCACCATCGCC	207855				

QY	2040	-----	2040
Db	208936	TCCTGTCTCTCCCAACACCCCTCTCTGCTTACTGTCTTTGGGAGCCCAACCCCTACC	208995
QY	2040	-----	2040
Db	208996	CCTAGCTTGGGTTCCTTACACCCCGGGTCCAGCCAGCTGGGAGGCAGCCCTGC	209055
QY	2041	-----	2041
Db	209056	CCCTGGGCTCCGAACCCCTGGGCGGGTCCGCTGACTCTGCACCCCGGCTGCTAGG	209115
QY	2042	YTyHisGlySerTyrSerProGluGlyValGluProValSerProValSerSerPr	2062
Db	209116	TTACACGGCAGCAGCTACAGCCCCCGAGGGGTGGAGCCGCTCAGCCCTGTGAGCTCAC	209175
QY	2062	oSerLeuThrHisAspLysGlyLeuProLysHisLeuGluGluLeuAspLysSerHisLe	2082
Db	209176	CAGTCTGACCCACGACAAGGGGCTCCCAAGCACCTGGAAGAGCTCGACAAGAGCCACCT	209235
QY	2082	uGluGlyGluLeuArgProLysGlnPro-----	2091
Db	209236	GGAGGGGAGCTGCGGCCCAAGCAGCCAGTACGCCCCACCCAGTACCCAGGCCCCCGAA	209295
QY	2091	-----	2091
Db	209296	GCCTTGACAGTGAGGACCCTCAAGGCCCATCATGCAGATAGGAAACAGAGGTGCCTA	209355
QY	2091	-----	2091
Db	209356	AAGGCCAAGGAATGGCTGGATCATGAGGCTCAAGGCTGAGGGCTGGGATTTGGGCCCA	209415
QY	2092	-----	2092
Db	209416	GCAGCCCTGGGGCCAGCAGACACCCCTGACCGACTCTGCTGCTGCGAGGCCCCGTGA	209475
QY	2095	ysLeuGlyGlyGluAlaHisLeuProHisLeuArgProLeuProGluSerGlnProS	2115
Db	209476	AGCTTGGGGGAGGCGGCCACCTCCACACCTGCGCGCTGCTGCTGAGAGCCAGCCCT	209535
QY	2115	erSerProLeuLeuGlnThrAlaProGlyValLysGlyHisGlnArgValThrL	2135
Db	209536	CGTCAGCCGCTGCTCCAGACCCCGCCGAGGGTCAAGAGTCAACAGCGGTGCTCACCC	209595
QY	2135	euAlaGlnHisIleSer-----	2140
Db	209596	TGGCCACGACATCAGTGAACCTAGCGGTTCTCTGCTGCTGCTGTGTCAACCTTTGCACCTG	209655
QY	2140	-----	2140
Db	209656	GGGGCACCGCCTGGAGAGGGATGGGAACCCACAGCCCTTCTGCTGCGGGGTG	209715
QY	2140	-----	2140
Db	209716	GCTGGGGATCCAGGGATGCGCTGGGGGATCCAGGGCTGGGTGAGGTGAGATCCC	209775
QY	2140	-----	2140
Db	209776	AAAGCCCGAGCAGCGGCACCATCACCGCCCCCTAATCCATGGGAGGAGCCTGTGATGCG	209835
QY	2140	-----	2140
Db	209836	AGCCGATGGCATCTTCAGGGCAATGAGGCTTCTGCTGCGCCAGGTTTCTCAGTGTCA	209895
QY	2140	-----	2140
Db	209896	TGGGCTGGTCTCATCAGCCATCTGCCAACTACAGCTTGGGACGCTGACACAGCCCCA	209955
QY	2140	-----	2140
Db	209956	CTCCATGCACACTGGGACAGGAGGCCAGAGGGTGGCGGCGAGGTCCACAGTCAACCA	210015
QY	2140	-----	2140

Db	210016	GGAAGCTGGCCCCCAGGATTTCTGCCCGAGCTCCGTCTAGCCCTCCCCACCCCCAG	210075
QY	2141	-----	2141
Db	210076	AAGGTTCTGTACGAGAGTGCTGCTGACTTGGGGCCCCCCTTGTCTGCTGAGGAGGTC	210135
QY	2143	IlleThrGlnAspTyrThrArgHisHisProGlnGlnLeuSerAlaProLeuProAlaPro	2162
Db	210136	ATCACACAGGACTACACCGGCACACCCACACAGCAGCTCAGCGACCCCTGCCGCCCC	210195
QY	2163	LeuTyrSerPheProGlyAlaSerCysProValLeuAspLeuArgArgProProSerAsp	2182
Db	210196	CTCTACTCTCTCCCTGGGGCAGCTGCCCGCTCTGGACCTCCGCGCCACCCAGTGCAC	210255
QY	2183	LeuTyrLeuProProProAspHisGlyAlaProAlaArgGlySerProHisSerGluGly	2202
Db	210256	CTCTACTCTCCCGCCCGGACCATGTGTGCCCGGCCCTGGGTCCCGCCACAGCGAAGG	210315
QY	2203	GlyLys-----	2204
Db	210316	GGCAAGAGGTGAGCGAGGATGGGGTGCTCTTGTGTGTGCTGAGCCGGCGGAGGCTTCG	210375
QY	2204	-----	2204
Db	210376	TCAGTCTCTGCTCAGAGTGGGTCTGAGCTCAGCTGCATATGAGGCCCGCTGTGTGCC	210435
QY	2204	-----	2204
Db	210436	ATTGCACAGCAAGAAATGGAGGCTCCAGGAGATGGGGAGTCCAGAGCGGATACATAA	210495
QY	2204	-----	2204
Db	210496	CGAATAATAGCTGATGAAGTACATGCTGTGCTCAGTGGGTTCCAGGCACTCAGGTGTAC	210555
QY	2204	-----	2204
Db	210556	CCTTTACACACAGCCCCCAGGAGACATAGGAGCATTTCTCCCAATTTACAGATGAAGA	210615
QY	2204	-----	2204
Db	210616	AACCTAAGGCTGGAGAAAGTGAATTAATTCACTTGGCCACAGGGGCACAGTCAGTGTGACAGA	210675
QY	2204	-----	2204
Db	210676	GGGGGATTTGTTCCAGGCTGTATGATTAGAGAGCAGCTTTCCACACATGCACACCCAC	210735
QY	2204	-----	2204
Db	210736	ACATATGCGCACACACACATGSCACACCCGCAACATGCGCACCCGCAACACACAGCT	210795
QY	2204	-----	2204
Db	210796	GCACACGCACACATGGCGGCGCACACATGSCACACCCGCAACATGGCGCGGCACAC	210855
QY	2204	-----	2204
Db	210856	ACATATGCACACCCGCAACATGCGCACACACATGCACACCCGCAACACAGGCGCACCC	210915
QY	2204	-----	2204
Db	210916	GCACACCCCTGTAGACACAGGCACATGSCATGCTCAOGCACACTCCCACTCCACCCCC	210975
QY	2204	-----	2204
Db	210976	GCCCCACCCCCCTGGTGAACCGTGGGGCTCTGGGGGTCAAAAGAGAAAGAGAGGG	211035
QY	2204	-----	2204
Db	211036	GAGGGCCCTGAGCTCCAGGGTGAAGGAGGCGTTTGTGGGGGGGGGGTAAATGTGT	211095
QY	2204	-----	2204

Db 211096 GTGGAGGACAGACATGGCAAGACAGCAGGACATCTTTGGGGGGGCGAGTGTGTAGCTGGC 211155
Qy 2204 ----- 2204
Db 211156 ACTGGGTACACAGAAATTCAGAGCAGGGGTCAATAAATCTGTGGCCCATGGGCCAGATC 211215
Qy 2204 ----- 2204
Db 211216 TAGCCCGGGCCCTCTGTGTGTACAATTCATGAACCTAAATAAATGATTTTACATTTTAA 211275
Qy 2204 ----- 2204
Db 211276 GGGTTGTTAAAAAATAAATAATGATAACGATACATCCAGAGATTACTTGTGTGTG 211335
Qy 2204 ----- 2204
Db 211336 AATAAGCTAAACGTTTATGATTTGGCCACGTACAGGAAGCGTGTGGGGCCCTGGTT 211395
Qy 2204 ----- 2204
Db 211396 TAGAGTGGAGGAGGGTGGCCCCCTCAGTAGGAGACCTCTGACCACATCTGGGGCCCT 211455
Qy 2205 ----- ArgSerProGluProAsnLysThrSerValLeuGlyGlyGluAspG1 2221
Db 211456 TTCTCCATCCAGGTCTCCAGAGCAAAACAAGACGTGGTCTTGGGTGGTGGTGGAGACGG 211515
Qy 2221 YileGluProValSerProGluGlyMetThrGluProGlyHisSerArgSerAlaVa 2241
Db 211516 TATTGAACCTGTCTCCACCGGAGGCGCATGACGGAGCCAGGCACTCCCGGAGTGCTGT 211575
Qy 2241 lTyrProLeuLysThrArgSerGlyGluGlnThrGluProSer----- 2255
Db 211576 GTACCGCTGCTGTACCGGATGGGAACAGACGGAGCCCAAG-GTACTTCTGTGGGCACA 211634
Qy 2255 ----- 2255
Db 211635 TGGCTGCCCCCGGATGCTCTGTGTATCCCTTGGCCATCTTGGCCCCAGTCCACCGTGG 211694
Qy 2255 ----- 2255
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Qy 2255 ----- 2255
Db 211755 AGGTTTCACTTGGGGGTGTATATATGCCACCCTCCCTGGGGAGACCTCAGTGGT 211814
Qy 2255 ----- 2255
Db 211815 AGCTTTCCATGCTTTGGGCTGGGATCTCAGCTGGACGAGCCCGTGTGACAGCCCTGT 211874
Qy 2255 ----- 2255
Db 211875 TGAACCTCTAAGAAATATAGCTAGTGTGTGGGCCACAGCGGGGGCGATGGGTGAGG 211934
Qy 2255 ----- 2255
Db 211935 TGGGACCTGAGAGGAAGCTGGGCCCGCTGCCCTGGGGAAGGCGATGATCGGAACCCAA 211994
Qy 2255 ----- 2255
Db 211995 TTTTCACTTTGGGGCTCTCTTGAGAGGGTTCAGGCTGGAGCAAGTGTGACAGGCGAGCC 212054
Qy 2255 ----- 2255
Db 212055 ACCAGGACCGCGGTCTCCCAAGACACCCCTAGCCCCAGGAGGGTGAACCGCAGAGG 212114
Qy 2255 ----- 2255
Db 212115 AGATTTTCAAGGCGGTATCTTACCAGGCGAGGGATGACGGCTGGGGCGGGTGAAG 212174
Qy 2255 ----- 2255
Db 212175 CTTGCTTCAAAATGTCTAAGGCATCTCAGGTGGTGTATTTCCCATCATCAAGGCGATGCA 212234

Qy 2256 ----- ArgMetGlySerLy 2260
Db 212235 AGCTCGGCACCAAGTGAGCTGATGTGAGGTGTTTGTATCTCTCACAGCAGGATGGGCTCAA 212294
Qy 2260 sSerProGlyAsnThrSerGlnProProAlaPhePheSerLysLeuThrGluSerAsnSe 2280
Db 212295 GTCTCCAGGCAACACCAGCCAGCCGCGGCTCTTCTCAGCAAGCTGACCGAGAGCAACTC 212354
Qy 2280 rAlaMetValLysSerLysLysGlnGluLeuAsnLysLeuAsnThrHisAsnArgAs 2300
Db 212355 CGCATGGTCAAGTCCAAAGCAAGAGATCAACAGAGCTGAACACCCCAACCCGAA 212414
Qy 2300 nGluProGluTyrAsnLysSerGlnProGlyThrGluLeuPheAsnMetProAlaIleTh 2320
Db 212415 TGAGCTGATACATAGTAAGGGGCTGCAGGCTCCCGGGGAAGCATGGGCCACAGGTGG 212474
Qy 2320 rGly 2321
Db 212475 CGGG 212478

RESULT 17

US-09-920-300A-485
; Sequence 485, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 485
; LENGTH: 520
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-485

Alignment Scores:

Pred. No.:	4,96e-37	Length:	520
Score:	746.50	Matches:	141
Percent Similarity:	91.95%	Conservative:	19
Best Local Similarity:	81.03%	Mismatches:	13
Query Match:	5.65%	Indels:	1
DB:	9	Gaps:	1

US-09-522-753-5 (1-2517) x US-09-920-300A-485 (1-520)

Qy 285 LysArgArgAsnHisAlaArgLysGlnTrpLysGlnLysPheCysGlnArgTyrAspGln 304
Db 1 AAAAGAAGAAATCATGCAAGAAACAAAGGCAAAAAATCTGCCAGCGTTATGATCAG 60
Qy 305 LeuMetGluAlaLeuGlnLysLysValGluArgIleGluAsnAsnProArgArgAla 324
Db 61 CTATCGAGCATGGGAGAAAAAAGTGACAGAAATAGAAAAATATCTCGAGGAAAGCT 120
Qy 325 LysGluSerLysValArgLysValArgLysGlnPheProGluLeuArgLysGlnArg 344
Db 121 AAAGAAGCAAAACAGAGGATATCTATGAAGAGCTTTCAGAAATTCGAAACAAGA 180
Qy 345 GluLeuGlnGluArgMetGlnSerArgValGlyGlnArgGlySerGlyLeuSerMetSer 364
Db 181 GAACAGCAAGAAAGATTTCAG---CGAGTTGGGAGAGGGAGCTGCTCTTCAGCCACC 237
Qy 365 AlaAlaArgSerGluHisGluValSerGluLeuIleAspGlyLeuSerGluGlnGluAsn 384
Db 238 ATTGCTAGGAGTAGCATGATTTCTTGAATTAATTGATGGGCTCTCTGAGCAGGAGAA 297

